

SCORE Search Results Details for Application 10679580 and Search Result us-10-679-580a-1.rni.

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This page gives you Search Results detail for the Application 10679580 and Search Result us-10-679-580a-1.rni.

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OM nucleic - nucleic search, using sw model

Run on: July 22, 2006, 22:47:34 ; Search time 2065 Seconds
(without alignments)
6110.779 Million cell updates/sec

Title: US-10-679-580A-1
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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1	1815.6	26.9	4173	4	US-09-512-581D-3	Sequence 3, Appli
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3	1815.6	26.9	5355	4	US-09-512-581D-4	Sequence 4, Appli
4	1808	26.8	4418	3	US-09-949-016-4088	Sequence 4088, Ap
5	1686.6	25.0	1722	3	US-09-023-655-121	Sequence 121, App
6	437.6	6.5	452	3	US-09-513-999C-34334	Sequence 34334, A
7	206	3.1	1195	3	US-09-270-767-13950	Sequence 13950, A
8	161	2.4	295	3	US-09-513-999C-2815	Sequence 2815, Ap
9	149.4	2.2	351	3	US-09-471-276-620	Sequence 620, App
10	131	1.9	192506	3	US-09-949-016-15830	Sequence 15830, A
c 11	130.2	1.9	530	3	US-09-328-111-682	Sequence 682, App
12	88.4	1.3	601	3	US-09-949-016-144642	Sequence 144642,
13	86.4	1.3	601	3	US-09-949-016-144587	Sequence 144587,
c 14	80.2	1.2	612	3	US-09-902-540-1357	Sequence 1357, Ap
c 15	77.8	1.2	7218	2	US-08-232-463-14	Sequence 14, Appl
c 16	75.6	1.1	1039	3	US-09-902-540-1280	Sequence 1280, Ap
c 17	72.8	1.1	19124	2	US-08-487-826B-13	Sequence 13, Appl
18	72.6	1.1	1141	3	US-09-806-708B-22	Sequence 22, Appl
19	69.6	1.0	601	3	US-09-949-016-144594	Sequence 144594,
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c 38	61.6	0.9	191569	3	US-09-949-016-15940	Sequence 15940, A
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45	57.4	0.9	601	3	US-09-949-016-145868	Sequence 145868,

ALIGNMENTS

RESULT 1

US-09-512-581D-3

; Sequence 3, Application US/09512581D

; Patent No. 6994992

; GENERAL INFORMATION:

; APPLICANT: Soto, Ana M.

; APPLICANT: Sonnenschein, Carlos

; APPLICANT: Geck, Peter

; APPLICANT: Szelei, Jozsef

; TITLE OF INVENTION: NOVEL ANDROGEN-INDUCED SUPPRESSOR OF CELL PROLIFERATION AND USES

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; TITLE OF INVENTION:  THEREOF
; FILE REFERENCE:  34724-026
; CURRENT APPLICATION NUMBER:  US/09/512,581D
; CURRENT FILING DATE:   2000-02-24
; PRIOR APPLICATION NUMBER:  US 60/121,461
; PRIOR FILING DATE:  1999-02-24
; NUMBER OF SEQ ID NOS:  72
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
;   LENGTH: 4173
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: (1)..(4173)
US-09-512-581D-3
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Matches 2457;  Conservative 0;  Mismatches 1069;  Indels 0;  Gaps 0;
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OM nucleic - nucleic search, using sw model

Run on: July 24, 2006, 01:59:18 ; Search time 36612 Seconds
(without alignments)
11779.237 Million cell updates/sec

Title: US-10-679-580A-1
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Gapop 10.0 , Gapext 1.0

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	4	3145.2	46.6	4809	11	AJ851547	AJ851547 Gallus ga
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	6	2612.8	38.7	137481	12	AC027207	AC027207 Homo sapi
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	13	2198	32.6	2212	2	AX881562	AX881562 Sequence
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	15	2134.2	31.6	5275	6	AK172992	AK172992 Mus muscu
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ALIGNMENTS

RESULT 1

AF294791

LOCUS AF294791 6744 bp mRNA linear PRI 22-MAR-2004

DEFINITION Homo sapiens SCC-112 (SCC-112) mRNA, complete cds.

ACCESSION AF294791

VERSION AF294791.1 GI:21951801
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE 1 (bases 1 to 6744)
 AUTHORS Kumar,D., Sakabe,I., Patel,S., Zhang,Y., Ahmad,I., Gehan,E.A.,
 Whiteside,T.L. and Kasid,U.
 TITLE SCC-112, a novel cell cycle-regulated molecule, exhibits reduced
 expression in human renal carcinomas
 JOURNAL Gene 328, 187-196 (2004)
 PUBMED 15019998
 REFERENCE 2 (bases 1 to 6744)
 AUTHORS Kumar,D. and Kasid,U.
 TITLE Direct Submission
 JOURNAL Submitted (09-AUG-2000) Radiation, Medicine, 3970 Reservoir Rd, NW,
 Washington, DC 20007, USA

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ORIGIN

Query Match 100.0%; Score 6744; DB 5; Length 6744;
 Best Local Similarity 100.0%; Pred. No. 0;
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Db	961	ATGCCACAGCTTGAATTCAACTAAAGAGCAATGATGGAGAAGAGCGATTAGCTGTTGTT	1020
Qy	1021	CGACTTCTAGCTAAATTGTTTGGCTCCAAAGATTCTGATTTGGCAACACAGAATCGTCCT	1080
Db	1021	CGACTTCTAGCTAAATTGTTTGGCTCCAAAGATTCTGATTTGGCAACACAGAATCGTCCT	1080
Qy	1081	CTTTGGCAATGTTTCTTGACGATTAAATGATATTCATGTTCTGTGAGATTAGAAAGT	1140
Db	1081	CTTTGGCAATGTTTCTTGACGATTAAATGATATTCATGTTCTGTGAGATTAGAAAGT	1140
Qy	1141	GTGAAATTTGCCAGTCATTGTTAAATGAATCAACCAGATTTAGCGAAGGATCTCACAGAA	1200
Db	1141	GTGAAATTTGCCAGTCATTGTTAAATGAATCAACCAGATTTAGCGAAGGATCTCACAGAA	1200
Qy	1201	TATTTAAAGGTTAGATCACATGATCCAGAAGAAGCTATTCGTATGATGTCATTGTTACT	1260
Db	1201	TATTTAAAGGTTAGATCACATGATCCAGAAGAAGCTATTCGTATGATGTCATTGTTACT	1260
Qy	1261	ATAATAACAGCTGCCAAGAGGGACCTGGCCTTAGTAAATGATCAGCTGCTTGGCTTTGTA	1320
Db	1261	ATAATAACAGCTGCCAAGAGGGACCTGGCCTTAGTAAATGATCAGCTGCTTGGCTTTGTA	1320
Qy	1321	AGGGAAAGAACACTGGATAAAACGGTGGCGAGTAAGAAAAGAAGCTATGATGGGTCTGGCT	1380
Db	1321	AGGGAAAGAACACTGGATAAAACGGTGGCGAGTAAGAAAAGAAGCTATGATGGGTCTGGCT	1380
Qy	1381	CAGCTTTATAAGAAATACTGTCTTCATGGTGAAGCAGGAAAGGAAGCTGCAGAGAAAGTC	1440
Db	1381	CAGCTTTATAAGAAATACTGTCTTCATGGTGAAGCAGGAAAGGAAGCTGCAGAGAAAGTC	1440
Qy	1441	AGCTGGATAAAAGGACAAACTTCTGCATATTTATTATCAGAACAGCATTGACGACAAACTG	1500
Db	1441	AGCTGGATAAAAGGACAAACTTCTGCATATTTATTATCAGAACAGCATTGACGACAAACTG	1500
Qy	1501	TTGGTAGAGAAAATCTTTGCTCAGTATCTTGTCCCCACAACCTGGAAACAGAAGAGAGA	1560
Db	1501	TTGGTAGAGAAAATCTTTGCTCAGTATCTTGTCCCCACAACCTGGAAACAGAAGAGAGA	1560
Qy	1561	ATGAAATGCTTATATTACTTATATGCTAGTTTGGATCCAAATGCTGTAAAAGCTCTCAAC	1620
Db	1561	ATGAAATGCTTATATTACTTATATGCTAGTTTGGATCCAAATGCTGTAAAAGCTCTCAAC	1620
Qy	1621	GAAATGTGGAAGTGTGAGAACATGCTTCGGAGCCATGTACGCGAACTATTGGATTGTCAC	1680
Db	1621	GAAATGTGGAAGTGTGAGAACATGCTTCGGAGCCATGTACGCGAACTATTGGATTGTCAC	1680
Qy	1681	AAGCAGCCTACATCAGAGGCTAACTGTTCTGCCATGTTTGGAAAACCTGATGACCATAGCA	1740
Db	1681	AAGCAGCCTACATCAGAGGCTAACTGTTCTGCCATGTTTGGAAAACCTGATGACCATAGCA	1740
Qy	1741	AAGAATTTGCCTGACCCCGGGAAAGCACAAGATTTTGTGAAGAAATTAACCAGGTTCTC	1800
Db	1741	AAGAATTTGCCTGACCCCGGGAAAGCACAAGATTTTGTGAAGAAATTAACCAGGTTCTC	1800
Qy	1801	GGCGATGATGAGAACTTCGGTCTCAGTTGGAGTTATTAATTAGCCCAACCTGTTCTTGC	1860

SCORE Search Results Details for Application 10679580 and Search Result us-10-679-580a-1.rng.

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OM nucleic - nucleic search, using sw model

Run on: July 24, 2006, 00:55:58 ; Search time 3752 Seconds
(without alignments)
12532.208 Million cell updates/sec

Title: US-10-679-580A-1
Perfect score: 6744
Sequence: 1 ggacctcgcaggccaagaat.....aaaccaagaaatgcagcatt 6744

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_8:*
1: geneseqn1980s:*
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3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
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8: geneseqn2003as:*
9: geneseqn2003bs:*
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12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	6744	100.0	6744	8	ABX14056	Abx14056 cDNA enco
2	6744	100.0	6744	14	ADX06262	Adx06262 Cyclin-de
3	6555.6	97.2	6956	8	ACC72031	Acc72031 BCU0720 g
4	5385.8	79.9	5469	6	ABQ99271	Abq99271 Human cod
5	5177	76.8	5177	14	AED18329	Aed18329 Fibrotic
6	5177	76.8	5177	15	AEF74956	Aef74956 Human pol
7	3875.4	57.5	3957	3	AAA47423	Aaa47423 Sequence
8	2198	32.6	2212	4	AAH17132	Aah17132 Human cDN
9	2128.4	31.6	2295	4	AAS02396	Aas02396 Human sec
10	1983.2	29.4	2002	4	AAH14767	Aah14767 Human cDN
11	1953.4	29.0	2496	6	ABK35358	Abk35358 Human cDN
12	1823.6	27.0	7473	5	ABV25469	Abv25469 Human pro
13	1822	27.0	5309	15	AEF74563	Aef74563 Human pol
14	1822	27.0	7444	13	ADR25694	Adr25694 Breast ca
15	1822	27.0	7473	5	ABV22430	Abv22430 Human pro
16	1822	27.0	7473	5	ABV28244	Abv28244 Human pro
17	1815.6	26.9	5271	3	AAA28051	Aaa28051 Human and
18	1815.6	26.9	5355	3	AAA28052	Aaa28052 Human and
19	1706.2	25.3	2265	11	ADM03755	Adm03755 Human cDN
20	1706.2	25.3	2265	14	AEC86685	Aec86685 Human cDN
21	1686.6	25.0	1722	11	ADI30795	Adi30795 Human cDN
22	1686.6	25.0	1722	13	ADS82862	Ads82862 Human lym
23	1489	22.1	1489	4	AAH18066	Aah18066 Human cDN
24	1148.8	17.0	1217	3	AAF18338	Aaf18338 Lung canc
25	726.8	10.8	785	4	AAH07766	Aah07766 Human cDN
26	686.4	10.2	1104	6	ABS56684	Abs56684 Euchromos
27	670.4	9.9	4128	13	ADR08232	Adr08232 Full leng
28	666.8	9.9	772	4	AAH03894	Aah03894 Human cDN
29	593.2	8.8	663	4	AAH07307	Aah07307 Human cDN
c 30	581.4	8.6	584	6	ABK44862	Abk44862 cDNA enco
c 31	478.6	7.1	542	4	AAH09415	Aah09415 Human cDN
c 32	462.2	6.9	512	4	AAH12296	Aah12296 Human cDN
33	437.6	6.5	452	3	AAC30259	Aac30259 Human sec
c 34	430.8	6.4	495	4	AAH12739	Aah12739 Human cDN
c 35	429.8	6.4	471	9	ACH16302	Ach16302 Human adu
36	417.2	6.2	434	8	ABZ17884	Abz17884 S2 subtra
37	408	6.0	408	6	ABV95661	Abv95661 Human pan
c 38	389.2	5.8	391	6	ABL38139	Abl38139 Human col
39	381	5.6	413	9	ACH49024	Ach49024 Human leu
40	376.8	5.6	422	9	ACH48906	Ach48906 Human leu
c 41	360.2	5.3	376	6	ABL37597	Abl37597 Human col
42	359	5.3	2416	12	ADO35588	Ado35588 Novel mou
c 43	346.2	5.1	706	10	ADD35009	Add35009 Mouse mit
44	335.2	5.0	380	14	AEE11851	Aee11851 Hamster c
45	335.2	5.0	380	14	AEE15493	Aee15493 Hamster S

ALIGNMENTS

RESULT 1

ABX14056

ID ABX14056 standard; cDNA; 6744 BP.

XX

AC ABX14056;

XX
DT 24-FEB-2003 (first entry)
XX
DE cDNA encoding human SCC-112 tumour supressor gene.
XX
KW ss; gene; human; chromosome 4p14; SCC-112; cancer; apoptosis; allodynia;
KW degenerative disorder; metastasis inhibition; breast cancer; causalgia;
KW kidney cancer; bladder cancer; pancreatic cancer; colon cancer;
KW squamous cell carcinoma; head trauma; spinal cord injury; herpes zoster;
KW global and focal ischaemic and haemorrhagic stroke; epilepsy; neuralgia;
KW hypoxia-induced nerve cell damage; anxiety; diabetes mellitus;
KW cardiac arrest; spinal cord lesion; stomach cancer; lung cancer;
KW neonatal distress; Alzheimer's disease; uterine cancer; colon cancer;
KW multiple sclerosis; phantom limb pain; hyperalgesia; Down's syndrome;
KW Huntington's disease; Parkinson's disease; Korsakoff's syndrome;
KW amyotrophic lateral sclerosis; cell survival; cell proliferation;
KW tumour supressor.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 232. .4125
FT /*tag= a
FT /product= "Human SCC-112"
FT polyA_signal 6721. .6726
FT /*tag= b
FT /standard_name= "PolyA signal"
XX
PN WO200281641-A2.
XX
PD 17-OCT-2002.
XX
PF 08-APR-2002; 2002WO-US010850.
XX
PR 06-APR-2001; 2001US-0281780P.
XX
PA (GEOU) UNIV GEORGETOWN.
XX
PI Kasid UN, Kumar D, Ahmad I;
XX
DR WPI; 2003-103330/09.
DR P-PSDB; ABG72803.
XX
PT New isolated SSC (undefined) tumor suppressor polypeptides and
PT polynucleotides, useful for diagnosing, preventing or treating cancer or
PT degenerative disease, e.g. Alzheimer's Disease, Huntington's disease, or
PT multiple sclerosis.
XX
PS Claim 1; Fig 1B; 83pp; English.
XX
CC The invention relates to a new isolated polypeptide SCC-112. The SCC-112
CC polypeptides and polynucleotides are useful for diagnosing, preventing or
CC treating cancer (e.g. breast cancer, kidney cancer, bladder cancer,
CC pancreatic cancer, colon cancer, squamous cell carcinoma, uterine cancer,
CC stomach cancer, colon cancer, lung cancer); or degenerative disease or
CC disorder (e.g. global and focal ischaemic and haemorrhagic stroke, head
CC trauma, spinal cord injury, hypoxia-induced nerve cell damage, nerve cell
CC damage caused by cardiac arrest or neonatal distress, epilepsy, anxiety,
CC diabetes mellitus, multiple sclerosis, phantom limb pain, causalgia,
CC neuralgias, herpes zoster, spinal cord lesions, hyperalgesia, allodynia,
CC Alzheimer's disease, Huntington's disease, Parkinson's disease,

CC amyotrophic lateral sclerosis, Down's syndrome and Korsakoff's syndrome).
CC The polypeptides and polynucleotides are also useful for inducing
CC apoptosis in cancer cells, increasing survival or proliferation of a
CC cell, or inhibiting cancer cell proliferation and/or metastasis in a
CC cancer patient. The polynucleotides can be used as probes to detect
CC complementary nucleotide sequences, or as primers to obtain additional
CC copies of the polynucleotides. SSC-112 may also be used for identifying
CC drugs for treatment of cancers. The present sequence represents cDNA
CC encoding the human SCC-112 tumour supressor gene which is located on
CC chromosome 4p14

XX
SQ Sequence 6744 BP; 2156 A; 1243 C; 1400 G; 1945 T; 0 U; 0 Other;

Query Match 100.0%; Score 6744; DB 8; Length 6744;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6744; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GGACCTCGCAGGCCAAGAATTCGGCACGAGGGGCGCCGGCTCCCGGGGCACGGACGGCCG	60
Db	1	GGACCTCGCAGGCCAAGAATTCGGCACGAGGGGCGCCGGCTCCCGGGGCACGGACGGCCG	60
Qy	61	GGCGCGCGCCTCTGCGAGGGGCGTCCGGTCCGAGTCGGCGGTCCGGGCCGGCGCGAGGT	120
Db	61	GGCGCGCGCCTCTGCGAGGGGCGTCCGGTCCGAGTCGGCGGTCCGGGCCGGCGCGAGGT	120
Qy	121	GCGTGCGGGCGGGCCGCGGGGGTCCCGACGGACACAAGCGCACACACTCCCGGAAGATC	180
Db	121	GCGTGCGGGCGGGCCGCGGGGGTCCCGACGGACACAAGCGCACACACTCCCGGAAGATC	180
Qy	181	GCTTACCCTCCGGGGGTAAAAGAGATCACCGACAAGATCACCACGGACGAGATGATCAAA	240
Db	181	GCTTACCCTCCGGGGGTAAAAGAGATCACCGACAAGATCACCACGGACGAGATGATCAAA	240
Qy	241	CGCCTGAAGATGGTAGTGAAAACCTTTATGGATATGGATCAGGACTCAGAAGATGAAAAA	300
Db	241	CGCCTGAAGATGGTAGTGAAAACCTTTATGGATATGGATCAGGACTCAGAAGATGAAAAA	300
Qy	301	CAGCAGTATCTCCCACTAGCCTTGATCTTGCATCTGAATTCTTCCTCAGGAACCCCAAT	360
Db	301	CAGCAGTATCTCCCACTAGCCTTGATCTTGCATCTGAATTCTTCCTCAGGAACCCCAAT	360
Qy	361	AAAGATGTGCGTCTCCTTGATGATGTTGTTGGCTGATATCTTTCGTATCTATGCCCCA	420
Db	361	AAAGATGTGCGTCTCCTTGATGATGTTGTTGGCTGATATCTTTCGTATCTATGCCCCA	420
Qy	421	GAAGCTCCATATACTTCCCATGATAAACTTAAGGACATATTTTGTATTATTACCAGACAA	480
Db	421	GAAGCTCCATATACTTCCCATGATAAACTTAAGGACATATTTTGTATTATTACCAGACAA	480
Qy	481	TTAAAAGGTTTGGAGGATACAAAGAGTCCACAGTTTAATAGATACTTTATTTATTAGAG	540
Db	481	TTAAAAGGTTTGGAGGATACAAAGAGTCCACAGTTTAATAGATACTTTATTTATTAGAG	540
Qy	541	AATTTAGCTTGGGTAAATCATATAACATCTGCTTTGAATTGGAAGATTGCAATGAAATT	600
Db	541	AATTTAGCTTGGGTAAATCATATAACATCTGCTTTGAATTGGAAGATTGCAATGAAATT	600
Qy	601	TTTATTCAGCTTTTGTAGAACTCTCTCTCAGTGATCAACAATAGCCACAATAAGAAGGTA	660
Db	601	TTTATTCAGCTTTTGTAGAACTCTCTCTCAGTGATCAACAATAGCCACAATAAGAAGGTA	660

Qy	661	CAAATGCACATGCTAGATTGATGAGTTCTATCATCATGGAAGGTGATGGAGTTACTCAA	720
Db	661	CAAATGCACATGCTAGATTGATGAGTTCTATCATCATGGAAGGTGATGGAGTTACTCAA	720
Qy	721	GAATTATTGGGCTCCATTCTTATTAACCTCATTCCTGCACATAAGAACTTAAATAAACAG	780
Db	721	GAATTATTGGGCTCCATTCTTATTAACCTCATTCCTGCACATAAGAACTTAAATAAACAG	780
Qy	781	TCCTTTGACCTTGCAAAAGTGCTATTGAAAAGAACAGTCCAGACTATTGAGGCATGCATT	840
Db	781	TCCTTTGACCTTGCAAAAGTGCTATTGAAAAGAACAGTCCAGACTATTGAGGCATGCATT	840
Qy	841	GCCAAATTTTTCAATCAAGTCCTGGTGCTGGGAAGATCATCAGTAAGTGATTGTTCAGAA	900
Db	841	GCCAAATTTTTCAATCAAGTCCTGGTGCTGGGAAGATCATCAGTAAGTGATTGTTCAGAA	900
Qy	901	CATGTATTTGATCTGATTTCAGGAACTTTTTGCTATAGATCCTCATTTATTATTATCCGTC	960
Db	901	CATGTATTTGATCTGATTTCAGGAACTTTTTGCTATAGATCCTCATTTATTATTATCCGTC	960
Qy	961	ATGCCACAGCTTGAATTCAAATAAGAGCAATGATGGAGAAGAGCGATTAGCTGTTGTT	1020
Db	961	ATGCCACAGCTTGAATTCAAATAAGAGCAATGATGGAGAAGAGCGATTAGCTGTTGTT	1020
Qy	1021	CGACTTCTAGCTAAATTGTTTGGCTCCAAAGATTCTGATTTGGCAACACAGAATCGTCCT	1080
Db	1021	CGACTTCTAGCTAAATTGTTTGGCTCCAAAGATTCTGATTTGGCAACACAGAATCGTCCT	1080
Qy	1081	CTTTGGCAATGTTTCTTGGACGATTTAATGATATTCATGTTCTGTGAGATTAGAAAGT	1140
Db	1081	CTTTGGCAATGTTTCTTGGACGATTTAATGATATTCATGTTCTGTGAGATTAGAAAGT	1140
Qy	1141	GTGAAATTTGCCAGTCATTGTTTAATGAATCACCCAGATTTAGCGAAGGATCTCACAGAA	1200
Db	1141	GTGAAATTTGCCAGTCATTGTTTAATGAATCACCCAGATTTAGCGAAGGATCTCACAGAA	1200
Qy	1201	TATTTAAAGGTTAGATCACATGATCCAGAAGAAGCTATTCGTATGATGTCATTGTTACT	1260
Db	1201	TATTTAAAGGTTAGATCACATGATCCAGAAGAAGCTATTCGTATGATGTCATTGTTACT	1260
Qy	1261	ATAATAACAGCTGCCAAGAGGGACCTGGCCTTAGTAAATGATCAGCTGCTTGGCTTTGTA	1320
Db	1261	ATAATAACAGCTGCCAAGAGGGACCTGGCCTTAGTAAATGATCAGCTGCTTGGCTTTGTA	1320
Qy	1321	AGGGAAAGAACACTGGATAAACGGTGGCGAGTAAGAAAAGAAGCTATGATGGGTCTGGCT	1380
Db	1321	AGGGAAAGAACACTGGATAAACGGTGGCGAGTAAGAAAAGAAGCTATGATGGGTCTGGCT	1380
Qy	1381	CAGCTTTATAAGAAATACTGTCTTCATGGTGAAGCAGGAAAGGAAGCTGCAGAGAAAGTC	1440
Db	1381	CAGCTTTATAAGAAATACTGTCTTCATGGTGAAGCAGGAAAGGAAGCTGCAGAGAAAGTC	1440
Qy	1441	AGCTGGATAAAGGACAAACTTCTGCATATTTATTATCAGAACAGCATTGACGACAAACTG	1500
Db	1441	AGCTGGATAAAGGACAAACTTCTGCATATTTATTATCAGAACAGCATTGACGACAAACTG	1500
Qy	1501	TTGGTAGAGAAAATCTTTGCTCAGTATCTTGTCCCCACAACCTGGAAACAGAAGAGAGA	1560
Db	1501	TTGGTAGAGAAAATCTTTGCTCAGTATCTTGTCCCCACAACCTGGAAACAGAAGAGAGA	1560
Qy	1561	ATGAAATGCTTATATTACTTATATGCTAGTTTGGATCCAAATGCTGTAAAAGCTCTCAAC	1620

Db	1561	 ATGAAATGCTTATATTACTTATATGCTAGTTTGGATCCAAATGCTGTAAAAGCTCTCAAC	1620
Qy	1621	GAAATGTGGAAGTGTGAGAACATGCTTCGGAGCCATGTACGCGAACTATTGGATTTGCAC	1680
Db	1621	 GAAATGTGGAAGTGTGAGAACATGCTTCGGAGCCATGTACGCGAACTATTGGATTTGCAC	1680
Qy	1681	AAGCAGCCTACATCAGAGGCTAACTGTTCTGCCATGTTTGGAAGAACTGATGACCATAGCA	1740
Db	1681	 AAGCAGCCTACATCAGAGGCTAACTGTTCTGCCATGTTTGGAAGAACTGATGACCATAGCA	1740
Qy	1741	AAGAATTTGCCTGACCCCGGGAAGCACAAGATTTTGTGAAGAAATTTAACCAGGTTCTC	1800
Db	1741	 AAGAATTTGCCTGACCCCGGGAAGCACAAGATTTTGTGAAGAAATTTAACCAGGTTCTC	1800
Qy	1801	GGCGATGATGAGAACTTCGGTCTCAGTTGGAGTTATTAATTAGCCCAACCTGTTCTTGC	1860
Db	1801	 GGCGATGATGAGAACTTCGGTCTCAGTTGGAGTTATTAATTAGCCCAACCTGTTCTTGC	1860
Qy	1861	AAACAAGCAGATATTTGTGTGAGAGAAATAGCCCGGAACTTGCAAATCCTAAGCAACCA	1920
Db	1861	 AAACAAGCAGATATTTGTGTGAGAGAAATAGCCCGGAACTTGCAAATCCTAAGCAACCA	1920
Qy	1921	ACAAATCCTTTTCTAGAGATGGTCAAATTTCTGTTGAAAGAATCGCACCTGTGCACATT	1980
Db	1921	 ACAAATCCTTTTCTAGAGATGGTCAAATTTCTGTTGAAAGAATCGCACCTGTGCACATT	1980
Qy	1981	GATTCAGAAGCCATAAGTGCACTAGTGAATTTGATGAATAAGTCAATAGAGGGGACAGCA	2040
Db	1981	 GATTCAGAAGCCATAAGTGCACTAGTGAATTTGATGAATAAGTCAATAGAGGGGACAGCA	2040
Qy	2041	GATGATGAAGAGGAGGGTGTAAGTCCAGATACAGCTATCCGTTGAGGACTTGAACCTCTT	2100
Db	2041	 GATGATGAAGAGGAGGGTGTAAGTCCAGATACAGCTATCCGTTGAGGACTTGAACCTCTT	2100
Qy	2101	AAGGTTCTGTCTTTTACACATCCTACCTCGTTCCACTCTGCAGAGACATATGAGTCCTTG	2160
Db	2101	 AAGGTTCTGTCTTTTACACATCCTACCTCGTTCCACTCTGCAGAGACATATGAGTCCTTG	2160
Qy	2161	TTACAGTGCCTAAGAATGGAGGATGACAAGGTAGCAGAAGCTGCTATTCAAATTTTGTAGA	2220
Db	2161	 TTACAGTGCCTAAGAATGGAGGATGACAAGGTAGCAGAAGCTGCTATTCAAATTTTGTAGA	2220
Qy	2221	AATACAGGTCAAAAATAGAAACAGACCTTCCCAGATACGATCGACCTTAATTCCCATT	2280
Db	2221	 AATACAGGTCAAAAATAGAAACAGACCTTCCCAGATACGATCGACCTTAATTCCCATT	2280
Qy	2281	TTACATCAAAAAGCAAAGAGGGGTACTCCACACCAAGCAAAAACAGGCTGTGCACTGTATA	2340
Db	2281	 TTACATCAAAAAGCAAAGAGGGGTACTCCACACCAAGCAAAAACAGGCTGTGCACTGTATA	2340
Qy	2341	CACGCCATATTCAAAAATAAGAAGTCCAGCTTGACAGATTTTGTAGCCACTCAGTAGG	2400
Db	2341	 CACGCCATATTCAAAAATAAGAAGTCCAGCTTGACAGATTTTGTAGCCACTCAGTAGG	2400
Qy	2401	AGTCTGAATGCTGATGTGCCAGAACTTATAACTCCATTAGTTTCATTGGGCCACATT	2460
Db	2401	 AGTCTGAATGCTGATGTGCCAGAACTTATAACTCCATTAGTTTCATTGGGCCACATT	2460
Qy	2461	TCTATGTTAGCACCAGATCAGTTTGCTTCCCAATGAAATCTGTAGTAGCAAATTTTATT	2520

Db	2461	TCTATGTTAGCACCAGATCAGTTTGCTTCCCCAATGAAATCTGTAGTAGCAAAATTTTATT	2520
Qy	2521	GTGAAAGATCTGCTAATGAATGACAGGTCAACAGGTGAAAAGAATGGAAAACCTGTGGTCT	2580
Db	2521	GTGAAAGATCTGCTAATGAATGACAGGTCAACAGGTGAAAAGAATGGAAAACCTGTGGTCT	2580
Qy	2581	CCAGATGAAGAGGTTTCCCCTGAAGTACTAGCAAAGGTACAGGCAATTAACTTCTGGTA	2640
Db	2581	CCAGATGAAGAGGTTTCCCCTGAAGTACTAGCAAAGGTACAGGCAATTAACTTCTGGTA	2640
Qy	2641	AGGTGGCTGTTGGGTATGAAAAACAACCAGTCTAAATCTGCCAATTCAACCCCTTCGGTTA	2700
Db	2641	AGGTGGCTGTTGGGTATGAAAAACAACCAGTCTAAATCTGCCAATTCAACCCCTTCGGTTA	2700
Qy	2701	TTATCAGCGATGTTGGTTAGTGAGGGTGACCTGACAGAGCAAAAGAGGATCAGTAAATCT	2760
Db	2701	TTATCAGCGATGTTGGTTAGTGAGGGTGACCTGACAGAGCAAAAGAGGATCAGTAAATCT	2760
Qy	2761	GATATGTCTCGCTTGGATTAGCTGCTGGTAGTGCCATAATGAAGCTTGCTCAGGAACCT	2820
Db	2761	GATATGTCTCGCTTGGATTAGCTGCTGGTAGTGCCATAATGAAGCTTGCTCAGGAACCT	2820
Qy	2821	TGTTACCATGAAATTATTACCCAGAACAGTTTCAGCTCTGTGCACTTGTTATTAATGAT	2880
Db	2821	TGTTACCATGAAATTATTACCCAGAACAGTTTCAGCTCTGTGCACTTGTTATTAATGAT	2880
Qy	2881	GAGTGTTACCAAGTAAGGCAGATAATTTGCTCAGAAGCTGCATAAGGCACCTGTGAAGTTA	2940
Db	2881	GAGTGTTACCAAGTAAGGCAGATAATTTGCTCAGAAGCTGCATAAGGCACCTGTGAAGTTA	2940
Qy	2941	CTGCTCCCATTTGGAGTATATGGCGATCTTTGCCTTGTTGCGCAAAGATCCTGTGAAGGAG	3000
Db	2941	CTGCTCCCATTTGGAGTATATGGCGATCTTTGCCTTGTTGCGCAAAGATCCTGTGAAGGAG	3000
Qy	3001	AGAAGAGCACACGCACGACAATGTTTACTGAAAAATATCAGTATACGCAGGGAATACATT	3060
Db	3001	AGAAGAGCACACGCACGACAATGTTTACTGAAAAATATCAGTATACGCAGGGAATACATT	3060
Qy	3061	AAGCAGAATCCTATGGCTACTGAGAAATTATTATCACTGTTGCCTGAATATGTAGTTCCA	3120
Db	3061	AAGCAGAATCCTATGGCTACTGAGAAATTATTATCACTGTTGCCTGAATATGTAGTTCCA	3120
Qy	3121	TACATGATTACCTGCTAGCCCATGATCCAGATTTTACAAGATCACAAGATGTTGATCAG	3180
Db	3121	TACATGATTACCTGCTAGCCCATGATCCAGATTTTACAAGATCACAAGATGTTGATCAG	3180
Qy	3181	CTTCGTGATATCAAAGAGTGCCTATGGTTCATGCTTGAAGTTTAAATGACAAAGAATGAA	3240
Db	3181	CTTCGTGATATCAAAGAGTGCCTATGGTTCATGCTTGAAGTTTAAATGACAAAGAATGAA	3240
Qy	3241	AACAATAGCCATGCCTTTATGAAGAAGATGGCAGAGAACATCAAGTTAACCAGAGATGCC	3300
Db	3241	AACAATAGCCATGCCTTTATGAAGAAGATGGCAGAGAACATCAAGTTAACCAGAGATGCC	3300
Qy	3301	CAGTCTCCAGATGAATCCAAGACAAATGAAAAACTGTATACAGTATGTGATGTGGCTCTC	3360
Db	3301	CAGTCTCCAGATGAATCCAAGACAAATGAAAAACTGTATACAGTATGTGATGTGGCTCTC	3360
Qy	3361	TGTGTTATAAATAGTAAAAGTGCTTTGTGCAATGCAGATTCACCAAAGGACCCAGTCCTC	3420
Db	3361	TGTGTTATAAATAGTAAAAGTGCTTTGTGCAATGCAGATTCACCAAAGGACCCAGTCCTC	3420

Qy	3421	CCAATGAAATTTTACACAACCTGAAAAGGACTTCTGTAACGATAAGAGTTATATTTCA	3480
Db	3421	CCAATGAAATTTTACACAACCTGAAAAGGACTTCTGTAACGATAAGAGTTATATTTCA	3480
Qy	3481	GAAGAGACAAGAGTACTTCTGTTAACAGGAAAGCCAAAGCCTGCTGGAGTACTAGGTGCA	3540
Db	3481	GAAGAGACAAGAGTACTTCTGTTAACAGGAAAGCCAAAGCCTGCTGGAGTACTAGGTGCA	3540
Qy	3541	GTAAATAAGCCTTTATCAGCAACGGGAAGGAAACCTATGTTAGAAGCACTGGCACTGAG	3600
Db	3541	GTAAATAAGCCTTTATCAGCAACGGGAAGGAAACCTATGTTAGAAGCACTGGCACTGAG	3600
Qy	3601	ACTGGAAGCAATATTAATGTAAATTCAGAGCTGAACCTTCAACCGGAAATCGATCAAGG	3660
Db	3601	ACTGGAAGCAATATTAATGTAAATTCAGAGCTGAACCTTCAACCGGAAATCGATCAAGG	3660
Qy	3661	GAACAGAGTTCAGAGGCAGCAGAAACTGGAGTTAGTGAAAATGAAGAGAACCTGTGAGG	3720
Db	3661	GAACAGAGTTCAGAGGCAGCAGAAACTGGAGTTAGTGAAAATGAAGAGAACCTGTGAGG	3720
Qy	3721	ATTATTTTCAGTCACACCTGTAAAGAATATTGACCCAGTAAAGAATAAGGAAATTAATTCT	3780
Db	3721	ATTATTTTCAGTCACACCTGTAAAGAATATTGACCCAGTAAAGAATAAGGAAATTAATTCT	3780
Qy	3781	GATCAGGCTACCCAGGGCAACATCAGCAGTGACCGAGGAAAGAAAAGAACAGTAACAGCA	3840
Db	3781	GATCAGGCTACCCAGGGCAACATCAGCAGTGACCGAGGAAAGAAAAGAACAGTAACAGCA	3840
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Db	3901	GCCCTTCCAAACCCAGGAGAGGACGTCGACCCAAGTCTGAATCTCAGGGCAATGCTACC	3960
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Db	5701	 GAAGTTTGAGAGTAAATGTCACTTACGTTTCTCATAGATGATCAAGAGTTGGCTGTGTAT	5760
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Db	5821	 TGCTTAGGGAACAATGGATACCAATGATAGAAAAATGATACCTTTACAGGGGCAGAAAAAT	5880
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Db	6001	 TGTGTTCTATTTAGAGAGAGTTTAAAGTTCTCTTAGCATCAGACAACTTGATTCTTAAGG	6060
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Db	6061	 TTTCCAGTGTGTCACCAACAAAAAGTGCATTGATAGGGACCTTTGTCTCTTCCTCCCTTT	6120
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Db      6721 AATAAAACCAAGAAATGCAGCATT 6744

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RESULT 2

ADX06262

ID ADX06262 standard; DNA; 6744 BP.

XX

AC ADX06262;

XX

DT 21-APR-2005 (first entry)

XX

DE Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 827.

XX

KW cytostatic; cyclin-dependent kinase; cdk; biomarker; gene; ds.

XX

OS Homo sapiens.

XX

PN WO2005012875-A2.

XX

PD 10-FEB-2005.

XX

PF 29-JUL-2004; 2004WO-US024424.
XX
PR 29-JUL-2003; 2003US-0490890P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;
XX
DR WPI; 2005-163068/17.
DR P-PSDB; ADX06263.
XX
PT Biomarkers useful for predicting or determining the response of a mammal
PT to a cancer treatment comprising administration of a modulator of cyclin-
PT dependent kinase activity.
XX
PS Claim 5; SEQ ID NO 827; 141pp; English.
XX
CC This invention describes a novel method of predicting or determining
CC whether a mammal will respond or is responding to an anti-cancer agent
CC that modulates cyclin-dependent kinase (cdk) activity. The method
CC comprises measuring the level of one or more biomarkers selected from
CC 2774 biomarkers given in the specification (nucleotide sequence SEQ ID
CC NO:1246 (Genbank EST W28729) is especially preferred). The method of the
CC invention is utilized in a kit for determining or predicting whether
CC patient would be susceptible or resistant to treatment by an agent
CC modulating cdk activity. The invention also describes a method for
CC utilizing individualized genetic profiles for treating diseases and
CC disorders based on patient's response and molecular level, specialized
CC microarrays comprising the biomarkers described, antibodies directed
CC against the biomarkers and a cell culture model to identify biomarkers.
CC The cdk modulator is preferably N-5-[[5-(1,1-Dimethylethyl)-2-
CC oxazolyl]methyl]thio]-2-thiazolyl-4-piperidine carboxamide, 0.5-L-
CC tartaric acid salt. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. This
CC sequence encodes a biomarker used in the method of the invention.
XX
SQ Sequence 6744 BP; 2156 A; 1243 C; 1400 G; 1945 T; 0 U; 0 Other;

Query Match 100.0%; Score 6744; DB 14; Length 6744;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6744; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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SCORE Search Results Details for Application 10679580 and Search Result us-10-679-580a-1.rst.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

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GenCore version 5.1.9

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OM nucleic - nucleic search, using sw model

Run on: July 24, 2006, 02:05:21 ; Search time 28579 Seconds
(without alignments)
13195.702 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: gb_est3:*
- 3: gb_est4:*
- 4: gb_est5:*
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- 6: gb_htc:*
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- 9: gb_est8:*
- 10: gb_est9:*
- 11: gb_gss1:*
- 12: gb_gss2:*
- 13: gb_gss3:*
- 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5070.6	75.2	5134	6	CR749425	CR749425 Homo sapi
2	3628.2	53.8	4019	14	DQ049835	DQ049835 Homo sapi
3	3385.8	50.2	4019	14	DQ049836	DQ049836 Pan trogl
4	932.4	13.8	2899	6	AK041682	AK041682 Mus muscu
5	865.2	12.8	939	3	BQ959509	BQ959509 AGENCOURT
6	852.8	12.6	1182	2	BM454791	BM454791 AGENCOURT
7	850.8	12.6	909	3	BU195798	BU195798 AGENCOURT
8	848.2	12.6	1088	2	BM475383	BM475383 AGENCOURT
9	845.8	12.5	923	3	BQ438312	BQ438312 AGENCOURT
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11	833.8	12.4	922	8	CR986733	CR986733 CR986733
12	832.2	12.3	1106	3	BM799673	BM799673 AGENCOURT
13	827.8	12.3	874	3	BU517176	BU517176 AGENCOURT
14	826.2	12.3	859	8	CR999562	CR999562 CR999562
15	819.8	12.2	991	2	BM470743	BM470743 AGENCOURT
16	817.4	12.1	867	3	BU159962	BU159962 AGENCOURT
17	814.6	12.1	1142	2	BM466282	BM466282 AGENCOURT
18	810	12.0	1002	2	BM465904	BM465904 AGENCOURT
19	808.8	12.0	835	9	DA735319	DA735319 DA735319
20	800.4	11.9	856	3	BU166770	BU166770 AGENCOURT
21	791.4	11.7	1056	2	BM477531	BM477531 AGENCOURT
22	782.6	11.6	3313	6	AK045159	AK045159 Mus muscu
23	776.4	11.5	792	8	CN430328	CN430328 170005322
24	770.8	11.4	853	3	BQ440349	BQ440349 AGENCOURT
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38	728	10.8	825	2	BI254793	BI254793 602974029
39	726.8	10.8	785	1	AU137328	AU137328 AU137328
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ALIGNMENTS

RESULT 1

CR749425

LOCUS CR749425 5134 bp mRNA linear HTC 17-APR-2005

DEFINITION Homo sapiens mRNA; cDNA DKFZp686B19246 (from clone DKFZp686B19246).

ACCESSION CR749425

VERSION CR749425.1 GI:51476560

KEYWORDS HTC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 5134)

AUTHORS Koehrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
Fobo,G., Han,M. and Wiemann,S.

CONSRTM The German cDNA Consortium

TITLE Direct Submission

JOURNAL Submitted (17-AUG-2004) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY

COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the
Heinrich-Heine-University, Duesseldorf/Germany) within the cDNA
sequencing consortium of the German Genome Project. This clone
(DKFZp686B19246) is available at the RZPD Deutsches
Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
<http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp686B19246>
Further information about the clone and the sequencing project is
available at <http://mips.gsf.de/projects/cdna/>.

FEATURES Location/Qualifiers

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DH10B; sites SfiIA + SfiIB"
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CDS 30. .3923
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SDLSEHVFDLIQELFAIDPHLLSVMPQLEFKLSNDGEERLAVVRL LAKLFGSKDSD
LATQNRPLWQCFLGRFNDIHVPVRLESVKFASHCLMNHPDLAKDLTEYLKVRSHDPEE
AIRHDVIVITIITAAKRD LALVNDQLLG FVRERTLDKRWRVRKEAMMGLAQLYKKYCLH
GEAGKEAAEKVSWIKDKLLHIYYQNSIDDKLLVEKIFAQYLVPHNLETEERMKCLYYL
YASLDPNAVKALNEMWKCQNMLRSHVRELLDLHKQPTSEANCSAMFGKLM TIAKNLPD
PGKAQDFVKKFNQVLGDDEKLRSQLELLISPTCSCKQADICVREIARKLANPKQPTNP
FLEMVKFLLERIAPVHIDSEAISALVKLMNKSIEGTADDEEEGVSPDTAIRSGLELLK
VLSFTHPTSFHSAETYESLLQCLRMEDDKVAEAAIQIFRNTGHK IETDLPQIRSTLIP
ILHQAKRGTPHQAKQAVHCIHAIFTNKEVQLAQIFEPLSRSLNADVPEQLITPLVSL
GHISMLAPDQFASPMKSVVANFIVKDLLMNDRSTGEKNGKLWSPDEEVSPEVLAKVQA
IKLLVRWLLGMKNNQSKSANSTLRLLSAMLVSEGLTEQKRISKSDMSRLRLAAGSAI

MKLAQEPYHEIITPEQFQLCALVINDECYQVRQIFAQKLHKALVKLLLPLEYMAIFA
 LCAKDPVKERRAHARQC LLKNISIRREYIKONPMATEKL LSLPEYVVPYMIHLAHD
 PDFTRSQDQDLRDIKECLWFMLEVLMTKNENNSHAFMKMAENIKLTRDAQSPDESK
 TNEKLYTVCDVALCVINSKALCNADSPKDPVLPKFFFTQPEKDFCNDKSYISEETRV
 LLLTGKPKPAGVLGAVNKPLSATGRKPYVRSTGTETG SNINVNSELNPSTGNRSREQS
 SEAAETGVSENEENPVRIISVTPVKNIDPVKNKEINSQATQGNISSDRGKKRTVTAA
 GAENIQKKTDEKVDSESGPPAPSKPRGRRRPKSESQGNATKNDDL NKPINKGRKRAAVG
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ORIGIN

Query Match 75.2%; Score 5070.6; DB 6; Length 5134;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 5085; Conservative 0; Mismatches 4; Indels 2; Gaps 1;

Qy	203	AGATCACCGACAAGATCACCGACGAGATGATCAAACGCCTGAAGATGGTAGTGAAAA	262
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Qy	263	CCTTTATGGATATGGATCAGGACTCAGAAGATGAAAAACAGCAGTATCTCCCACTAGCCT	322
Db	61	CCTTTATGGATATGGATCAGGACTCAGAAGATGAAAAACAGCAGTATCTCCCACTAGCCT	120
Qy	323	TGCATCTTGCATCTGAATTCTTCCTCAGGAACCCCAATAAAGATGTGCGTCTCCTTG TAG	382
Db	121	TGCATCTTGCATCTGAATTCTTCCTCAGGAACCCCAATAAAGATGTGCGTCTCCTTG TAG	180
Qy	383	CATGTTGTTTGGCTGATATCTTTCGTATCTATGCCCCAGAAGCTCCATATACTTCCCATG	442
Db	181	CATGTTGTTTGGCTGATATCTTTCGTATCTATGCCCCAGAAGCTCCATATACTTCCCATG	240
Qy	443	ATAAACTTAAGGACATATTTTTGT TTTATTACCAGACAATTAAGGTTTGAGGATACAA	502
Db	241	ATAAACTTAAGGACATATTTTTGT TTTATTACCAGACAATTAAGGTTTGAGGATACAA	300
Qy	503	AGAGTCCACAGTTTAATAGATACTTTTATTTATTAGAGAATTTAGCTTGGGTAAATCAT	562
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Qy	563	ATAACATCTGCTTTGAATTGGAAGATTGCAATGAAATTTTATTAGCTTTT TAGAACTC	622
Db	361	ATAACATCTGCTTTGAATTGGAAGATTGCAATGAAATTTTATTAGCTTTT TAGAACTC	420
Qy	623	TCTTCTCAGTGATCAACAATAGCCACAATAAGAAGGTACAAATGCACATGCTAGATT TGA	682
Db	421	TCTTCTCAGTGATCAACAATAGCCACAATAAGAAGGTACAAATGCACATGCTAGATT TGA	480
Qy	683	TGAGTTCTATCATCATGGAAGGTGATGGAGTTACTCAAGAATTATTGGGCTCCATTCTTA	742
Db	481	TGAGTTCTATCATCATGGAAGGTGATGGAGTTACTCAAGAATTATTGGGCTCCATTCTTA	540
Qy	743	TTAACCTCATTCTGACATAAGAAGCTTAAATAAACAGTCCTTTGACCTTGCAAAAGTGC	802
Db	541	TTAACCTCATTCTGACATAAGAAGCTTAAATAAACAGTCCTTTGACCTTGCAAAAGTGC	600
Qy	803	TATTGAAAAGAACAGTCCAGACTATTGAGGCATGCATTGCCAATTTTTTCAATCAAGTCC	862
Db	601	TATTGAAAAGAACAGTCCAGACTATTGAGGCATGCATTGCTAATTTTTTCAATCAAGTCC	660
Qy	863	TGGTGCTGGGAAGATCATCAGTAAGTGATTGTGTCAGAACATGTATTGATCTGATT CAGG	922
Db	661	TGGTGCTGGGAAGATCATCAGTAAGTGATTGTGTCAGAACATGTATTGATCTGATT CAGG	720

SCORE Search Results Details for Application 10679580 and Search Result us-10-679-580a-2.rag.

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OM protein - protein search, using sw model

Run on: July 21, 2006, 21:02:13 ; Search time 203 Seconds
(without alignments)
2921.230 Million cell updates/sec

Title: US-10-679-580A-2
Perfect score: 6650
Sequence: 1 MIKRLKMVVKTFMDMDQDSE.....KLQDLAKKAAPAERQIDLQR 1297

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Match	Length	DB	ID	Description

1	6650	100.0	1297	9	ADX06263	Adx06263	Cyclin-de
2	6643	99.9	1337	6	ABR58297	Abr58297	BCU0720 p
3	6618	99.5	1297	6	ABG72803	Abg72803	Human tum
4	4711	70.8	919	5	ABP64685	Abp64685	Human pro
5	4668.5	70.2	1391	3	AAV94702	Aay94702	Human and
6	4363	65.6	854	3	AAB01382	Aab01382	Neuron-as
7	3494	52.5	687	6	ABR58332	Abr58332	XM_047529
8	2842	42.7	600	7	ADM06198	Adm06198	Human pro
9	2842	42.7	600	9	AEC89128	Aec89128	Human cDN
10	2439.5	36.7	846	7	ADJ69898	Adj69898	Human hea
11	1911	28.7	1218	4	ABB67869	Abb67869	Drosophil
12	1861	28.0	363	3	AAB58462	Aab58462	Lung canc
13	1715	25.8	333	4	AAB94946	Aab94946	Human pro
14	1440.5	21.7	588	8	ADR10188	Adr10188	Human pro
15	1187	17.8	233	4	AAB95449	Aab95449	Human pro
16	910	13.7	182	5	ABB84560	Abb84560	Human euc
17	862	13.0	165	4	AAU01759	Aau01759	Human sec
18	759	11.4	161	4	AAU01760	Aau01760	Human sec
19	387	5.8	147	5	ABB89260	Abb89260	Human pol
20	377	5.7	92	3	AAG02811	Aag02811	Human sec
21	314	4.7	101	3	AAV65247	Aay65247	Human 5'
22	314	4.7	101	8	ADU72811	Adu72811	Signal pe
23	314	4.7	101	9	ADZ73802	Adz73802	Human inc
24	217.5	3.3	1743	2	AAW98879	Aaw98879	H. pylori
25	214.5	3.2	1875	6	ABR53560	Abr53560	Protein s
26	214.5	3.2	1875	7	ADK64380	Adk64380	Disease t
27	214.5	3.2	1875	8	ADS43855	Ads43855	Bacterial
28	213	3.2	761	8	ADX79770	Adx79770	Plant ful
29	204.5	3.1	1790	6	ABR53116	Abr53116	Protein s
30	204.5	3.1	1790	7	ADK63040	Adk63040	Disease t
31	204.5	3.1	1790	8	ADN18933	Adn18933	Bacterial
32	204.5	3.1	1790	9	ADY85285	Ady85285	Yeast hom
33	204	3.1	759	7	ABM88120	Abm88120	Rice abio
34	199.5	3.0	960	4	AAB94466	Aab94466	Human pro
35	199.5	3.0	1015	4	AAG64040	Aag64040	Human DRF
36	199.5	3.0	1015	9	ADY20095	Ady20095	PRO polyp
37	199.5	3.0	1015	9	ADY17460	Ady17460	PRO polyp
38	199.5	3.0	1160	4	ABB59418	Abb59418	Drosophil
39	199	3.0	2568	9	ADW44253	Adw44253	Human cen
40	199	3.0	2633	4	ABG06505	Abg06505	Novel hum
41	199	3.0	2663	4	AAM39097	Aam39097	Human pol
42	199	3.0	2663	8	ADQ17932	Adq17932	Human sof
43	199	3.0	2663	9	ADX06867	Adx06867	Cyclin-de
44	199	3.0	2688	4	AAM40883	Aam40883	Human pol
45	198.5	3.0	1927	6	ABU30805	Abu30805	Protein e

ALIGNMENTS

RESULT 1

ADX06263

ID ADX06263 standard; protein; 1297 AA.

XX

AC ADX06263;

XX

DT 21-APR-2005 (first entry)

XX

DE Cyclin-dependent kinase modulation biomarker SEQ ID NO 828.

XX

KW cytostatic; cyclin-dependent kinase; cdk; biomarker.
 XX
 OS Homo sapiens.
 XX
 PN WO2005012875-A2.
 XX
 PD 10-FEB-2005.
 XX
 PF 29-JUL-2004; 2004WO-US024424.
 XX
 PR 29-JUL-2003; 2003US-0490890P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;
 XX
 DR WPI; 2005-163068/17.
 DR N-PSDB; ADX06262.
 XX
 PT Biomarkers useful for predicting or determining the response of a mammal
 PT to a cancer treatment comprising administration of a modulator of cyclin-
 PT dependent kinase activity.
 XX
 PS Claim 5; SEQ ID NO 828; 141pp; English.
 XX
 CC This invention describes a novel method of predicting or determining
 CC whether a mammal will respond or is responding to an anti-cancer agent
 CC that modulates cyclin-dependent kinase (cdk) activity. The method
 CC comprises measuring the level of one or more biomarkers selected from
 CC 2774 biomarkers given in the specification (nucleotide sequence SEQ ID
 CC NO:1246 (Genbank EST W28729) is especially preferred). The method of the
 CC invention is utilized in a kit for determining or predicting whether
 CC patient would be susceptible or resistant to treatment by an agent
 CC modulating cdk activity. The invention also describes a method for
 CC utilizing individualized genetic profiles for treating diseases and
 CC disorders based on patient's response and molecular level, specialized
 CC microarrays comprising the biomarkers described, antibodies directed
 CC against the biomarkers and a cell culture model to identify biomarkers.
 CC The cdk modulator is preferably N-5-[[5-(1,1-Dimethylethyl)-2-
 CC oxazolyl]methyl]thio]-2-thiazolyl-4-piperidine carboxamide, 0.5-L-
 CC tartaric acid salt. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. This
 CC sequence represents a biomarker used in the method of the invention.
 XX
 SQ Sequence 1297 AA;

Query Match 100.0%; Score 6650; DB 9; Length 1297;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MIKRLKMVVKT FMDMDQDSEDEKQQYLPLALHLASEFFLRNPNKDVRLLVACCLADIFRI 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MIKRLKMVVKT FMDMDQDSEDEKQQYLPLALHLASEFFLRNPNKDVRLLVACCLADIFRI 60

 Qy 61 YAPEAPYTSHDKLKDIFLFITRQLKGLEDTKSPQFNRYFYLLLENLAWVKSYNICFELEDC 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 YAPEAPYTSHDKLKDIFLFITRQLKGLEDTKSPQFNRYFYLLLENLAWVKSYNICFELEDC 120

 Qy 121 NEIFIQLFRTLFSVINNSHNKKVQMHLDLMSIIMEGDGVTQELLGSILINLIPAHKNL 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db	121	NEIFIQLFRTLFSVINNSHNKKVQMHMLDLMSSI IMEGDGVTVQELLGSILINLI PAHKNL	180
Qy	181	NKQSFDLAKVLLKRTVQTI EACIANFFNQVLVLGRSSVSDLSEHVFDLIQELFAIDPHLL	240
Db	181	NKQSFDLAKVLLKRTVQTI EACIANFFNQVLVLGRSSVSDLSEHVFDLIQELFAIDPHLL	240
Qy	241	LSVMPQLEFKLKSNDGEERLAVVRL LAKLFGSKDSDLATQNRPLWQCFLGRFNDIHVPVR	300
Db	241	LSVMPQLEFKLKSNDGEERLAVVRL LAKLFGSKDSDLATQNRPLWQCFLGRFNDIHVPVR	300
Qy	301	LESVKFASHCLMNHPDLAKDLTEY LKVRSHDPEEAI RHDVIVTI ITAAKRDLALVNDQLL	360
Db	301	LESVKFASHCLMNHPDLAKDLTEY LKVRSHDPEEAI RHDVIVTI ITAAKRDLALVNDQLL	360
Qy	361	GFVRERTLDKRWRVRKEAMMGLAQ LYKKYCLHGEAGKEAAEKVSWIKDKLLHIYYQNSID	420
Db	361	GFVRERTLDKRWRVRKEAMMGLAQ LYKKYCLHGEAGKEAAEKVSWIKDKLLHIYYQNSID	420
Qy	421	DKLLVEKIFAQYLVPHNLETEERMKCLY YLYASLDPNAV KALNEMWKCQNMLRSHVRELL	480
Db	421	DKLLVEKIFAQYLVPHNLETEERMKCLY YLYASLDPNAV KALNEMWKCQNMLRSHVRELL	480
Qy	481	DLHKQPTSEANCSAMFGKLM TIAKNLDPGKAQDFVKKFNQVLGDDEKLRSQLELLISPT	540
Db	481	DLHKQPTSEANCSAMFGKLM TIAKNLDPGKAQDFVKKFNQVLGDDEKLRSQLELLISPT	540
Qy	541	CSCQQADICVREIARKLANPKQPTNPFLE MVKFLLERIAPVHIDSEAI SALVKLMNKSIE	600
Db	541	CSCQQADICVREIARKLANPKQPTNPFLE MVKFLLERIAPVHIDSEAI SALVKLMNKSIE	600
Qy	601	GTADDEEEGVSPDTAIRSGLELLKVLSF THPTSFHSAETYESLLQCLRMEDDKVAEAAIQ	660
Db	601	GTADDEEEGVSPDTAIRSGLELLKVLSF THPTSFHSAETYESLLQCLRMEDDKVAEAAIQ	660
Qy	661	IFRNTGHKIE TDL PQIRSTLIPILHQKAKRGTPHQAKQAVHCIHAI FTNKEVQLAQIFEP	720
Db	661	IFRNTGHKIE TDL PQIRSTLIPILHQKAKRGTPHQAKQAVHCIHAI FTNKEVQLAQIFEP	720
Qy	721	LSRSLNADVPEQLITPLVSLGHISMLAPDQFASPMKSVVANFIVKDLLMNDRSTGEKNGK	780
Db	721	LSRSLNADVPEQLITPLVSLGHISMLAPDQFASPMKSVVANFIVKDLLMNDRSTGEKNGK	780
Qy	781	LWSPDEEVSPEVLAKVQAIKLLVRWLLGMKN NQSKSANSTLRLLSAMLVSEGDLTEQKRI	840
Db	781	LWSPDEEVSPEVLAKVQAIKLLVRWLLGMKN NQSKSANSTLRLLSAMLVSEGDLTEQKRI	840
Qy	841	SKSDMSRLRLAAGSAIMKLAQEP CYHEIITPEQFQLCALVINDECYQVRQIFAQKLHKAL	900
Db	841	SKSDMSRLRLAAGSAIMKLAQEP CYHEIITPEQFQLCALVINDECYQVRQIFAQKLHKAL	900
Qy	901	VKLLLPLEYMAIFALCAKDPVKERRAHARQCL LKNI SIRREYIKQNPIMATEKLLSLLPEY	960
Db	901	VKLLLPLEYMAIFALCAKDPVKERRAHARQCL LKNI SIRREYIKQNPIMATEKLLSLLPEY	960
Qy	961	VVPYMIHLLAHDPDFTRSQDQDQLRDIKECL WFMLEVLMTKNENNSHAFMKKMAENIKLT	1020
Db	961	VVPYMIHLLAHDPDFTRSQDQDQLRDIKECL WFMLEVLMTKNENNSHAFMKKMAENIKLT	1020
Qy	1021	RDAQSPDESKTNEKLYTVCDVALCVINSK SALSALCNADSPKDPVLPMKFFTQPEKDFCNDKS	1080
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Qy      1081 YISEETRVLLLLTGKPKPAGVLGAVNKPLSATGRKPYVRSTGTETGSNINVNSELNPSTGN 1140
        |||
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Db      1141 RSREQSSEAAETGVSENEENPVRIISVTPVKNIDPVKNKEINSDQATQGNISSDRGKKRT 1200

Qy      1201 VTAAGAENIQQKTDEKVDSESGPPAPSKPRRGRRPKSESQGNATKNDDLKPKPINKGRKRAA 1260
        |||
Db      1201 VTAAGAENIQQKTDEKVDSESGPPAPSKPRRGRRPKSESQGNATKNDDLKPKPINKGRKRAA 1260

Qy      1261 VGQESPGGLEAGNAKAPKLQDLAKKAAPAERQIDLQR 1297
        |||
Db      1261 VGQESPGGLEAGNAKAPKLQDLAKKAAPAERQIDLQR 1297

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RESULT 2

ABR58297

ID ABR58297 standard; protein; 1337 AA.

XX

AC ABR58297;

XX

DT 08-JUL-2003 (first entry)

XX

DE BCU0720 protein #SEQ ID 40.

XX

KW Breast cancer; cytostatic; gene therapy; antisense therapy; regulated;
 KW drug discovery; clinical medicine; forensic medicine; chromosome 4p14.

XX

OS Homo sapiens.

XX

PN WO2003029421-A2.

XX

PD 10-APR-2003.

XX

PF 02-OCT-2002; 2002WO-US031287.

XX

PR 03-OCT-2001; 2001US-0326526P.

PR 14-MAY-2002; 2002US-00144194.

XX

PA (ORIG-) ORIGENE TECHNOLOGIES INC.

XX

PI Sun Z, Li X, Fan W, Kovacs KF, Jay G;

XX

DR WPI; 2003-381623/36.

DR N-PSDB; ACC72031.

XX

PT New isolated human differentially-regulated breast cancer polynucleotide
 PT and polypeptide, useful for diagnosing, staging, prognosticating,
 PT preventing and/or treating diseases and conditions relating to breast
 PT cancer.

XX

PS Claim 6; SEQ ID NO 40; 127pp + Sequence Listing; English.

XX

CC The invention relates to isolated polynucleotides which are
 CC differentially-regulated in breast cancer. The methods and compositions
 CC of the present invention are useful for detecting, diagnosing, staging,
 CC monitoring, prognosticating, preventing and/or treating diseases and
 CC conditions relating to breast cancer, and may be used in gene therapy or

XX
SQ Sequence 1337 AA;

Query Match 99.9%; Score 6643; DB 6; Length 1337;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1296; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

http://es/ScoreAccessWeb/GetItem.action?AppId=10679580&seqId=567833&ItemName=us-10-679-580a... 8/6/2006

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Qy      721 LSRSLNADVPEQLITPLVSLGHISMLAPDQFASPMKSVVANFIVKDLLMNRSTGEKNGK 780
      |||
Db      761 LSRSLNADVPEQLITPLVSLGHISMLAPDQFASPMKSVVANFIVKDLLMNRSTGEKNGK 820

Qy      781 LWSPDEEVSPPEVLAKVQAIKLLVRWLLGMKNNQSKSANSTLRLLSAMLVSEGDLTEQKRI 840
      |||
Db      821 LWSPDEEVSPPEVLAKVQAIKLLVRWLLGMKNNQSKSANSTLRLLSAMLVSEGDLTEQKRI 880

Qy      841 SKSDMSRLRLAAGSAIMKLAQEPYHEIITPEQFQLCALVINDECYQVRQIFAQKLHKAL 900
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Db      881 SKSDMSRLRLAAGSAIMKLAQEPYHEIITPEQFQLCALVINDECYQVRQIFAQKLHKAL 940

Qy      901 VKLLLPLEYMAIFALCAKDPVKERRAHARQCLLKNISIRREYIKQNPIMATEKLLSLLPEY 960
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Db      941 VKLLLPLEYMAIFALCAKDPVKERRAHARQCLLKNISIRREYIKQNPIMATEKLLSLLPEY 1000

Qy      961 VVPYMIHLLAHDPDFTRSQDQDLRDIKECLWFMLEVLMTKNENNSHAFMKKMAENIKLT 1020
      |||
Db     1001 VVPYMIHLLAHDPDFTRSQDQDLRDIKECLWFMLEVLMTKNENNSHAFMKKMAENIKLT 1060

Qy     1021 RDAQSPDESKTNEKLYTVCDVALCVINSKSALCNADSPKDPVLPMKFFTQPEKDFCNDKS 1080
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Qy     1081 YISEETRVLLLLTGKPKPAGVLGAVNKPLSATGRKPYVRSTGTETGSNINVNSELNPSTGN 1140
      |||
Db     1121 YISEETRVLLLLTGKPKPAGVLGAVNKPLSATGRKPYVRSTGTETGSNINVNSELNPSTGN 1180

Qy     1141 RSREQSSEAAETGVSENEENPVRIISVTPVKNIDPVKNKEINSDQATQGNISSDRGKKRT 1200
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Db     1181 RSREQSSEAAETGVSENEENPVRIISVTPVKNIDPVKNKEINSDQATQGNISSDRGKKRT 1240

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      |||
Db     1241 VTAAGAENIQQKTDEKVDSEGPAPSKPRRGRRPKSESQGNATKNDDLNPINKGRKRAA 1300

Qy     1261 VGQESPGGLEAGNAKAPKLQDLAKKAAPAERQIDLQR 1297
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Db     1301 VGQESPGGLEAGNAKAPKLQDLAKKAAPAERQIDLQR 1337

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RESULT 3

ABG72803

ID ABG72803 standard; protein; 1297 AA.

XX

AC ABG72803;

XX

DT 24-FEB-2003 (first entry)

XX

DE Human tumour supressor SCC-112.

XX

KW Human; SCC-112; cancer; apoptosis; allodynia; cell proliferation;

KW degenerative disorder; metastasis inhibition; breast cancer; causalgia;

KW kidney cancer; bladder cancer; pancreatic cancer; colon cancer;

KW squamous cell carcinoma; head trauma; spinal cord injury; herpes zoster;

KW global and focal ischaemic and haemorrhagic stroke; epilepsy; neuralgia;

KW hypoxia-induced nerve cell damage; anxiety; diabetes mellitus;

KW cardiac arrest; spinal cord lesion; lung cancer; tumour supressor;

KW neonatal distress; Alzheimer's disease; colon cancer; stomach cancer;

KW multiple sclerosis; phantom limb pain; hyperalgesia; Down's syndrome;

KW Huntington's disease; Parkinson's disease; Korsakoff's syndrome;
 KW amyotrophic lateral sclerosis; cell survival; uterine cancer.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 2. .137
 FT /label= RhoGEF domain
 FT Domain 127. .651
 FT /label= N-adaptin_domain
 FT Region 166. .187
 FT /label= Leucine_Zipper
 FT Domain 249. .350
 FT /label= SKP1_domain
 FT Region 597. .617
 FT /note= "PEST sequence site"
 FT Region 858. .865
 FT /note= "Tyrosine kinase phosphorylation site"
 FT Region 920. .926
 FT /note= "Nuclear localisation signature sequence"
 FT Region 1030. .1036
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 FT Region 1143. .1663
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 FT Region 1278. .1297
 FT /label= Epitope_region
 FT /note= "Residues 1278 to 1297 are specifically claimed in
 FT claim 41"
 XX
 PN WO200281641-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 08-APR-2002; 2002WO-US010850.
 XX
 PR 06-APR-2001; 2001US-0281780P.
 XX
 PA (GEOU) UNIV GEORGETOWN.
 XX
 PI Kasid UN, Kumar D, Ahmad I;
 XX
 DR WPI; 2003-103330/09.
 DR N-PSDB; ABX14056.
 XX
 PT New isolated SSC (undefined) tumor suppressor polypeptides and
 PT polynucleotides, useful for diagnosing, preventing or treating cancer or
 PT degenerative disease, e.g. Alzheimer's Disease, Huntington's disease, or
 PT multiple sclerosis.
 XX

XX

XX

Db 1 MIKRLKVVVKT FMDMDODSEDEKOOYLPLALHLASEFFLRNPKNKDVRLLVACCLADIFRI 60

Db 61 YAPEAPYTSHDKLKDIFLFITROLKGLEDTKSPQFNRYFYLLLENLAWVKSYNICFELEDC 120

Db 121 NEFIQLFRTLFSVINNSHNKKVOMHMLDLMSSIIMEGCGVTOELLGSILINLI PAHKNL 180

Db 181 NKOSFDLAKVLLKRTVOTIEACIANFFNOVLVLGRSSVSDLSEGVFDLIOELFAIDPHLL 240

Db 241 LSVMPQLEFKLKSNDGEERLAVVRLAKLFGSKDSDLATQNRPLWQCFLGRFNDIHVPVR 300

Db 301 LESVKFASHCLMNHPDLAKDLTEYLVKVRSHDPEEAIKRDVIVTIITAAKRDLALVNDQLL 360

Db 361 GFVRERTLDKRWRVRKEAMMGLAQLYKKYCLHGEAGKEAAEKVSWIKDKLLHIYYQNSID 420

Db 421 DKLLVEKIFAQYLVPHNLETEERMKCLYYLYASLDPNAVKALNEMWKCQNMLRSHVRELL 480

Qy	481	DLHKQPTSEANCSAMFGKLMTIAKNLPDPGKAQDFVKKFNQVLGDDEKLRSQLELLISPT	540
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Qy	541	CSCQADICVREIARKLANPKQPTNPFLEMVKFLLERIAPVHIDSEAI SALVKLMNKSIE	600
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Qy	601	GTADDEEEGVSPDTAIRSGLELLKVLSTHPTSFHSAETYESLLQCLRMEDDKVAEAAIQ	660
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Qy	661	IFRNTGHKIEIDLPIRSTLIPILHQKAKRGTPHQAKQAVHCIHAI FTNKEVQLAQIFEP	720
Db	661	IFRNTGHKIEIDLPIRSTLIPILHQKAKRGTPHQAKQAVHCIHAI FTNKEVQLAQIFEP	720
Qy	721	LSRSLNADVPEQLITPLVSLGHISMLAPDQFASPMKSVVANFIVKDLLMNDRSTGEKNGK	780
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Qy	781	LWSPDEEVSPEVLAKVQAIKLLVRWLLGMKNNQSKSANSTLRLLSAMLVSEGDLTEQKRI	840
Db	781	LWSPDEEVSPEVLAKVQAIKLLVRWLLGMKNNQSKSANSTLRLLSAMLVSEGDLTEQKRI	840
Qy	841	SKSDMSRLRLAAGSAIMKLAQEPYHEIITPEQFQCALVINDECYQVRQIFAQKLHKAL	900
Db	841	SKSDMSRLRLAAGSAIMKLAQEPYHEIITPEQFQCALVINDECYQVRQIFAQKLHKAL	900
Qy	901	VKLLLPLEYMAIFALCAKDPVKERRAHARQCLLKNISIRREYIKQNPMA TEKLLSLLPEY	960
Db	901	VKLLLPLEYMAIFALCAKDPVKERRAHARQCLLKNISIRREYIKQNPMA TEKLLSLLPEY	960
Qy	961	VVPYMIHLLAHDPDFTRSQDQDLRDIKECLWFMLEVLMTKNENNSHAFMKKMAENIKLT	1020
Db	961	VVPYMIHLLAHDPDFTRSQDQDLRDIKECLWFMLEVLMTKNENNSHAFMKKMAENIKLT	1020
Qy	1021	RDAQSPDESKTNEKLYTVCDAVLCVINSKSA LCNADSPKDPVLPMKFFTQPEKDFCNDKS	1080
Db	1021	RDAQSPDESKTNEKLYTVCDAVLCVINSKSA LCNADSPKDPVLPMKFFTQPEKDFCNDKS	1080
Qy	1081	YISEETRVLLL TGKPKPAGVLGAVNKPLSATGRKPYVRSTGTETGSNINVNSELNPSTGN	1140
Db	1081	YISEETRVLLL TGKPKPAGVLGAVNKPLSATGRKPYVRSTGTETGSNINVNSELNPSTGN	1140
Qy	1141	RSREQSSEAAETGVSENEENPVRIISVTPVKNIDPVKNKEINSDQATQGNISSDRGKKRT	1200
Db	1141	RSREQSSEAAETGVSENEENPVRIISVTPVKNIDPVKNKEINSDQATQGNISSDRGKKRT	1200
Qy	1201	VTAAGAENIQQKTDEKVDSESGPPAPSKPRRGRRPKSESQGNATKNDDL NKPINKGRKRAA	1260
Db	1201	VTAAGAENIQQKTDEKVDSESGPPAPSKPRRGRRPKSESQGNATKNDDL NKPINKGRKRAA	1260
Qy	1261	VGQESPGGLEAGNAKAPKLQDLAKKAAPAERQIDLQR	1297
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RESULT 4
ABP64685
ID ABP64685 standard; protein; 919 AA.
XX

AC ABP64685;
XX
DT 25-FEB-2003 (first entry)
XX
DE Human protein SEQ ID 345.
XX
KW Human; expressed sequence tag; EST; haematopoietic disorder;
KW central nervous system disease; viral infection;
KW peripheral nervous system disease; non-healing wound; infectious disease;
KW immune deficiency; immune disorder; bacterial infection; allergy; cancer;
KW fungal infection; autoimmune disorder; coagulation disorder; nootropic;
KW antiallergic; antiinflammatory; immunosuppressive; neuroprotective;
KW cytostatic; haemostatic; virucide; antibacterial; fungicide;
KW immunostimulant; cerebroprotective.
XX
OS Homo sapiens.
XX
PN WO200259260-A2.
XX
PD 01-AUG-2002.
XX
PF 16-NOV-2001; 2001WO-US042950.
XX
PR 17-NOV-2000; 2000US-00714936.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA;
PI Ren F, Xue AJ, Yang Y, Wehrman T, Drmanac RT;
XX
DR WPI; 2002-590824/63.
DR N-PSDB; ABQ99271.
XX
PT New isolated polynucleotide, useful in research, diagnostic or
PT therapeutic methods, e.g. preventing or treating disorders involving
PT aberrant protein expression or biological activity.
XX
PS Claim 20; SEQ ID NO 345; 394pp; English.
XX
CC The present invention relates to novel human coding sequences (ABQ99268-
CC ABQ99608) and proteins (ABP64682-ABP65022). The sequences are useful in
CC therapeutic, diagnostic and research methods. The polynucleotides may be
CC used in the field of molecular biology as hybridisation probes, primers
CC for PCR, for chromosome and gene mapping, for the recombinant production
CC of protein, or in generation of anti-sense DNA or RNA. The
CC polynucleotides are useful in diagnostics as expressed sequence tags
CC (ESTs) for identifying expressed genes or for physical mapping of the
CC human genome. The proteins may be used as molecular weight markers, or as
CC nutritional sources or supplements. The proteins may be used to maintain
CC and expand cell population in a totipotent or pluripotent state
CC useful for re-engineering damaged or diseased tissues, transplantation,
CC manufacture of bio-pharmaceuticals or the development of bio-sensors. The
CC polynucleotides and proteins are useful for preventing, treating or
CC ameliorating disorders involving aberrant protein expression or
CC biological activity, e.g. haematopoietic disorders, central/peripheral
CC nervous system diseases, mechanical and traumatic disorders, non-healing
CC wounds, immune deficiencies and disorders, infectious diseases caused by
CC viral, bacterial or fungal infection, autoimmune disorders, allergic
CC reactions and conditions, coagulation disorders, or cancer. The
CC polynucleotide sequences of the invention were assembled from ESTs
CC isolated mainly by sequencing by hybridisation, and in some cases,

CC sequences obtained from one or more public databases. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 919 AA;

Query Match 70.8%; Score 4711; DB 5; Length 919;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 919; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	379	MMGLAQLYKKYCLHGEAGKEAAEKVSWIKDKLLHIYYQNSIDDKLLVEKIFAQYLVPHNL	438
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Qy	439	ETEERMKCLYYLYASLDPNAVKALEMWKQCNMLRSHVRELLDLHKQPTSEANC SAMFGK	498
Db	61	ETEERMKCLYYLYASLDPNAVKALEMWKQCNMLRSHVRELLDLHKQPTSEANC SAMFGK	120
Qy	499	LMTIAKNLPDPGKAQDFVKKFNQVLGDDEKLRSQLLELLISPTCSCKQADICVREIARKLA	558
Db	121	LMTIAKNLPDPGKAQDFVKKFNQVLGDDEKLRSQLLELLISPTCSCKQADICVREIARKLA	180
Qy	559	NPKQPTNPFLEMVKFLLERIAIPVHIDSEAISALVKLMNKSIEGTADDEE EGVSPDTAIRS	618
Db	181	NPKQPTNPFLEMVKFLLERIAIPVHIDSEAISALVKLMNKSIEGTADDEE EGVSPDTAIRS	240
Qy	619	GLELLKVLSTHPTSFHSAETYESLLQCLRMEDDKVAEAAIQIFRNTGHKIETDLPQIRS	678
Db	241	GLELLKVLSTHPTSFHSAETYESLLQCLRMEDDKVAEAAIQIFRNTGHKIETDLPQIRS	300
Qy	679	TLIPILHQAKRGTPHQAKQAVHC IHAIFTNKEVQLAQIFEPLSRSLNADVPEQLITPLV	738
Db	301	TLIPILHQAKRGTPHQAKQAVHC IHAIFTNKEVQLAQIFEPLSRSLNADVPEQLITPLV	360
Qy	739	SLGHSMLAPDQFASPMKSVVANFIVKDLLMND RSTGEKNGKLWSPDEEVSP EVLAKVQA	798
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Qy	859	LAQEP CYHEIITPEQFQLCALVINDECYQVRQIFAQKLHKALVKLLLPLEYMAIFALCAK	918
Db	481	LAQEP CYHEIITPEQFQLCALVINDECYQVRQIFAQKLHKALVKLLLPLEYMAIFALCAK	540
Qy	919	DPVKERRAHARQCLLKNISIRREYIKQNP MATEKLLSLLPEYVVPYMIHLAHD PPFTRS	978
Db	541	DPVKERRAHARQCLLKNISIRREYIKQNP MATEKLLSLLPEYVVPYMIHLAHD PPFTRS	600
Qy	979	QDVDQLRDIKECLWFMLEVLMTKNENNSHAFMKKMAENIKLTRDAQSPDESKTNEKLYTV	1038
Db	601	QDVDQLRDIKECLWFMLEVLMTKNENNSHAFMKKMAENIKLTRDAQSPDESKTNEKLYTV	660
Qy	1039	CDVALCVINSKSALCNADSPKDPV LPMKFFTQPEKDFCNDKSYISEETRVLLLTGKPKPA	1098
Db	661	CDVALCVINSKSALCNADSPKDPV LPMKFFTQPEKDFCNDKSYISEETRVLLLTGKPKPA	720
Qy	1099	GVLGAVNKP L SATGRKP YVRSTGTETGSNINVNSELNPSTGNRSREQSSEAAETGVSENE	1158

SCORE Search Results Details for Application 10679580 and Search Result us-10-679-580a-2.rai.

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OM protein - protein search, using sw model

Run on: July 21, 2006, 21:11:59 ; Search time 55 Seconds
(without alignments)
2064.131 Million cell updates/sec

Title: US-10-679-580A-2
Perfect score: 6650
Sequence: 1 MIKRLKMVVKTfMDMDQDSE.....KLQDLAKKAAPAERQIDLQR 1297

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description	
1	4668.5	70.2	1391	2	US-09-512-581D-2	Sequence 2, Appli
2	4352.5	65.5	1346	2	US-09-949-016-9959	Sequence 9959, Ap

3	702	10.6	312	2	US-09-270-767-45520	Sequence 45520, A
4	377	5.7	92	2	US-09-513-999C-6892	Sequence 6892, Ap
5	374	5.6	309	2	US-09-270-767-45536	Sequence 45536, A
6	328.5	4.9	752	2	US-09-248-796A-15445	Sequence 15445, A
7	314	4.7	101	2	US-09-471-276-1408	Sequence 1408, Ap
8	284	4.3	235	2	US-09-270-767-43236	Sequence 43236, A
9	219	3.3	265	2	US-09-248-796A-15446	Sequence 15446, A
10	199	3.0	2663	2	US-09-538-092-1252	Sequence 1252, Ap
11	198	3.0	2662	2	US-09-595-684B-31	Sequence 31, Appl
12	195.5	2.9	3248	1	US-08-353-700-1	Sequence 1, Appli
13	195.5	2.9	3248	5	PCT-US95-16216-1	Sequence 1, Appli
14	191.5	2.9	2482	1	US-08-328-254-6	Sequence 6, Appli
15	190.5	2.9	3210	2	US-09-538-092-1154	Sequence 1154, Ap
16	189	2.8	1051	2	US-08-965-762-14	Sequence 14, Appl
17	189	2.8	1051	2	US-09-911-927-14	Sequence 14, Appl
18	189	2.8	1051	2	US-09-911-882-14	Sequence 14, Appl
19	189	2.8	1051	2	US-09-911-888-14	Sequence 14, Appl
20	181.5	2.7	169	2	US-09-270-767-33370	Sequence 33370, A
21	181.5	2.7	169	2	US-09-270-767-48587	Sequence 48587, A
22	181.5	2.7	2265	2	US-10-144-198-35	Sequence 35, Appl
23	180	2.7	2733	2	US-09-949-016-11433	Sequence 11433, A
24	177.5	2.7	3878	2	US-09-914-259-11	Sequence 11, Appl
25	177	2.7	2158	2	US-10-144-198-34	Sequence 34, Appl
26	177	2.7	2697	2	US-10-144-198-12	Sequence 12, Appl
27	176.5	2.7	1979	2	US-09-949-016-6468	Sequence 6468, Ap
28	176.5	2.7	2047	2	US-09-949-016-7404	Sequence 7404, Ap
29	176	2.6	1055	2	US-09-949-016-9776	Sequence 9776, Ap
30	175	2.6	3696	2	US-09-134-001C-5080	Sequence 5080, Ap
31	174	2.6	3259	2	US-09-949-016-6507	Sequence 6507, Ap
32	172	2.6	994	2	US-09-949-016-6779	Sequence 6779, Ap
33	172	2.6	1173	2	US-09-248-796A-19313	Sequence 19313, A
34	168	2.5	2704	2	US-09-538-092-1260	Sequence 1260, Ap
35	167.5	2.5	2954	2	US-09-150-867-1	Sequence 1, Appli
36	167.5	2.5	2954	3	US-09-724-584-1	Sequence 1, Appli
37	164.5	2.5	2101	1	US-08-466-390-4	Sequence 4, Appli
38	164.5	2.5	2101	1	US-08-470-950-4	Sequence 4, Appli
39	164.5	2.5	2101	1	US-08-467-781-4	Sequence 4, Appli
40	164.5	2.5	2101	1	US-08-195-487-4	Sequence 4, Appli
41	164.5	2.5	2101	1	US-08-483-924-4	Sequence 4, Appli
42	164.5	2.5	2101	2	US-09-452-294-1	Sequence 1, Appli
43	164.5	2.5	2101	2	US-09-296-662-32	Sequence 32, Appl
44	164.5	2.5	2101	5	PCT-US93-06160-4	Sequence 4, Appli
45	164.5	2.5	2115	2	US-09-296-662-33	Sequence 33, Appl

ALIGNMENTS

RESULT 1

US-09-512-581D-2

; Sequence 2, Application US/09512581D

; Patent No. 6994992

; GENERAL INFORMATION:

; APPLICANT: Soto, Ana M.

; APPLICANT: Sonnenschein, Carlos

; APPLICANT: Geck, Peter

; APPLICANT: Szelei, Jozsef

; TITLE OF INVENTION: NOVEL ANDROGEN-INDUCED SUPPRESSOR OF CELL PROLIFERATION AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 34724-026

; CURRENT APPLICATION NUMBER: US/09/512,581D

; CURRENT FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/121,461
 ; PRIOR FILING DATE: 1999-02-24
 ; NUMBER OF SEQ ID NOS: 72
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 2
 ; LENGTH: 1391
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-512-581D-2

Query Match 70.2%; Score 4668.5; DB 2; Length 1391;
 Best Local Similarity 69.0%; Pred. No. 0;
 Matches 908; Conservative 160; Mismatches 199; Indels 49; Gaps 11;

Qy	1	MIKRLKMVVKT	FMDMDQDSEDEKQ	QYLPLALHLASE	FFLRNP	NKDVRL	LVACCLADIFRI	60
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Db	31	MVRLKMVVKT	FMDMDQDSEEEKE	LYLNLALHLASD	FFLKHPGK	VDVRL	LVACCLADIFRI	90
Qy	61	YAPEAPYTS	HDKLKDI	FLFITRQLK	GLEDTKS	PQFNRY	FYLLENLAWVKS	120
Db	91	YAPEAPYTS	PDKLKDI	FMFITRQLK	GLEDTKS	PQFNRY	FYLLENIAWVKS	150
Qy	121	NEIFTQLF	RTLFSVIN	NSHNKQV	QMHL	DL	MSSII	180
Db	151	NEIFTQLY	RTLFSVIN	NGHNQKV	HMMV	DL	MSSII	210
Qy	181	NKQSF	DLAKVLLK	RVTQ	TEACIAN	FFNQVL	VLRSSV	240
Db	211	NKQAYD	LAKALLK	RTAQAI	EPYIT	TFNQV	LMGKTS	270
Qy	241	LSVMPQ	LEFKLKS	NDGEER	LAVR	LLAKL	FGSKD	300
Db	271	LSVLPQ	LEFKLKS	NDNEER	LQVVK	LLAKM	FGAKD	330
Qy	301	LESVKF	ASHCLM	NHPDLA	KDLTEY	LKVR	SHDPEE	360
Db	331	LECVKF	ASHCLM	NHPDLA	KDLTEY	LKVR	SHDPEE	390
Qy	361	GFVRE	RTLDK	RWRVR	KEAM	GLAQ	LYKKY	420
Db	391	NFVRE	RTLDK	RWRVR	KEAM	GLAQ	IYKKY	450
Qy	421	DKLLV	EKIFAQ	YLVPHN	LETE	ERMK	CLYYL	480
Db	451	DRLLV	ERIFAQ	YMVPHN	LET	ERMK	CLYYL	510
Qy	481	DLHKQ	P	SEANCS	AMFG	KLMT	IAKNL	540
Db	511	DLIKQ	P	KTASV	KAI	FSKVM	VITRNL	570
Qy	541	CSCQ	QADIC	VREI	ARKLAN	PKQPT	NPFLE	600
Db	571	CSCQ	AEGCV	REIT	TKKL	GNPK	QPTN	630
Qy	601	GTADDE	EEGV	SPD	TAIR	SGL	ELLK	660
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Db	691	IFKNTGSKIEEDFPHIRSALLPVLHHKSKKGPPRQAKYAIHCIHAIFSSKETQFAQIFEP	750
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Db	751	LHKSLDPSNLEHLITPLVTIGHIALAPDQFAAPWKSWSVATFIVKDLLMNDRLPGKKT	810
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Db	811	LWVPDEEVSPETMVKIQAIKMMVRWLLGMKNHNSKSGTSTLRLLTTILHSDGDLTEQGKI	870
Qy	841	SKSDMSRLRLAAGSAIMKLAQEPYHEIITPEQFQCALVINDECYQVRQIFAQKLHKAL	900
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Db	871	SKPDMSRLRLAAGSAIVKLAQEPYHEIITLEQYQLCALAINDECYQVRQVFAQKLHKGL	930
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Db	931	SRLRLPLEYMAICALCAKDPVKERRAHARQCLVKNI NVRREYLKQHA AVSEKLLSLLPEY	990
Qy	961	VVPYMIHLLAHDPDFTRSQDQDLRDIKECLWFMLEVLMTKNENNSHAFMKKMAENIKLT	1020
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Qy	1021	RDAQSPDESKTNEKLYTVCDVALCVINSKALCNADSPKDPVLPMKFFTQPEKDFCNDKS	1080
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Qy	1081	YISEETRVLLLTGKPKPAGVLGAVNKPLSATGRKPYVRSTGTETGSNINVNSELNPSTGN	1140
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Db	1169	RIKGR-LDSSEMDHSENE--YTMSSPLPGKSDKRDDSDLVRSELEKPRGRKKTPTVTEQ	1225
Qy	1180	E--INSDQAT-----QGNISSDRGKKRTVTAAGAENIQKQTEK-----VDESGPP	1223
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Db	1226	EEKLGMDDLTKLVQEQQPKGSQSRKRGRHTASESDE-QQWPEEKRLKEDILENEDEQNSP	1284
Qy	1224	APSKPRRGRRPKSESQGNATKNDDLKNPKINKGRKR---AAVGQESPGGLEAGNAK	1275
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Db	1285	-PKGKGRGRPPKPLG-GGT PKEEPTMKTSKKGSKKSGPPAPEEEEEERQSGNTE	1338

RESULT 2
US-09-949-016-9959
; Sequence 9959, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012

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This page gives you Search Results detail for the Application 10679580 and Search Result us-10-679-580a-2.rpr.
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OM protein - protein search, using sw model

Run on: July 21, 2006, 21:06:29 ; Search time 53 Seconds
(without alignments)
2354.588 Million cell updates/sec

Title: US-10-679-580A-2
Perfect score: 6650
Sequence: 1 MIKRLKMVVKTFMDMDQDSE.....KLQDLAKKAAPAERQIDLQR 1297

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	4350	65.4	851	2 T00374	hypothetical prote
2	661.5	9.9	1579	2 T23142	hypothetical prote
3	652	9.8	1506	2 S52957	bimD protein - Eme
4	621.5	9.3	1303	2 E96805	hypothetical prote
5	538	8.1	1277	2 S54451	hypothetical prote
6	257	3.9	390	2 T43647	hypothetical prote
7	256.5	3.9	780	2 F96840	hypothetical prote
8	250	3.8	990	2 H86293	protein T24D18.4 [

9	220	3.3	852	2	T06310	hypothetical prote
10	214.5	3.2	1875	2	S38173	myosin-like protei
11	204.5	3.1	1790	2	S67593	transport protein
12	203	3.1	1819	2	A71928	cag island protein
13	200.5	3.0	2139	2	T18296	myosin heavy chain
14	199	3.0	2663	1	S28261	centromere protein
15	198.5	3.0	1927	2	G64585	cag pathogenicity
16	196.5	3.0	1160	2	T13713	beta3 protein - fr
17	192	2.9	1679	2	S48385	hypothetical prote
18	191.5	2.9	1302	1	JC6009	surface-located me
19	190.5	2.9	1916	2	S46157	RIF1 protein - yea
20	190	2.9	2253	2	T30336	nuclear/mitotic ap
21	189	2.8	1051	2	S59791	probable membrane
22	188	2.8	1630	2	S64403	ESP1 protein - yea
23	185.5	2.8	4385	2	T29042	hypothetical prote
24	185	2.8	2297	2	AB2494	hypothetical prote
25	183.5	2.8	1721	2	T21214	hypothetical prote
26	182.5	2.7	2819	2	A90551	conserved hypothet
27	180.5	2.7	932	2	S65214	probable alpha/gam
28	180	2.7	3225	2	I52300	giantin - human
29	179.5	2.7	2346	2	T13829	Tpr homolog - frui
30	179	2.7	2116	2	A26655	myosin heavy chain
31	178	2.7	1034	2	T17458	chromosome condens
32	175.5	2.6	1642	2	T08880	NMDA receptor-bind
33	175.5	2.6	2493	2	S45734	probable membrane
34	174	2.6	2692	2	T23768	hypothetical prote
35	174	2.6	3259	1	A56539	giantin - human
36	173.5	2.6	1931	2	A59234	slow myosin heavy
37	173	2.6	798	2	I50479	neurofilament medi
38	173	2.6	1226	2	I51617	kinesin-like prote
39	172.5	2.6	1837	2	T41023	probable nuclear p
40	172	2.6	845	2	A45669	neurofilament trip
41	172	2.6	1727	2	T50073	myosin-like coiled
42	172	2.6	2481	2	D90011	FmtB protein [impo
43	170.5	2.6	1447	2	F82909	hypothetical prote
44	170.5	2.6	1864	2	F86378	protein F21J9.12 {
45	170.5	2.6	2415	1	A33733	spectrin alpha cha

ALIGNMENTS

RESULT 1

T00374

hypothetical protein KIAA0648 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004

C;Accession: T00374

R;Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O
DNA Res. 5, 169-176, 1998

A;Title: Prediction of the coding sequences of unidentified human genes. X. The complete sequences

A;Reference number: Z14142; MUID:98403880; PMID:9734811

A;Accession: T00374

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-851

A;Cross-references: UNIPROT:Q9Y4D4; UNIPARC:UPI000006D34B; EMBL:AB014548; NID:g3327109; PIDN:BAA31

A;Experimental source: brain

C;Genetics:

A;Note: KIAA0648

<http://es/ScoreAccessWeb/GetItem.action?AppId=10679580&seqId=567837&ItemName=us-10-679-580a-...> 8/6/2006

|||||||
Db 841 APAERQIDLQR 851

RESULT 2

T23142
hypothetical protein H38K22.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23142; T24139
R;Barlow, K.
submitted to the EMBL Data Library, June 1998
A;Reference number: Z19695
A;Accession: T23142
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1579
A;Cross-references: UNIPROT:Q9XTF6; UNIPARC:UPI0000078215; EMBL:AL024499; PIDN:CAA19710.1; GSPDB:GI
A;Experimental source: clone H38K22
R;Ainscough, R.
submitted to the EMBL Data Library, August 1995
A;Reference number: Z19843
A;Accession: T24139
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1579
A;Cross-references: UNIPARC:UPI0000078215; EMBL:Z50874; PIDN:CAA90774.1; GSPDB:GN00021; CESP:H38K2:
A;Experimental source: clone R10E4
C;Genetics:
A;Gene: CESP:H38K22.1
A;Map position: 3
A;Introns: 28/3; 99/3; 130/3; 239/3; 323/3; 363/2; 396/1; 444/3; 559/2; 651/3; 689/3; 793/1; 831/3

Query Match 9.9%; Score 661.5; DB 2; Length 1579;
Best Local Similarity 20.6%; Pred. No. 1.5e-28;
Matches 324; Conservative 288; Mismatches 616; Indels 345; Gaps 54;

Qy	2	IKRLKMVVKTFMDMDQDSEDE---KQQYLPLALHLASEFFLRNPNKDVRLLVACCLADIF	58
		: : : : : : : : : : : :	
Db	24	IERLRKLFNCLHDCKTNNSEEVS PNR FARLFQHLSEQECLDNSNTDFRILLSLCLANIL	83
Qy	59	RIYAPEAPYTSHDKLKDIFLFITRQLKGLEDT--KSPQFNRYFYLLLENLAWVKSYNICFE	116
		: : : : : : : : : : :	
Db	84	RIFQPELPTPSVMDLKEVYIYLFRTMRGLGDTVQDSPKFKNYFSLVETME--KIIPPIIE	141
Qy	117	LEDCNE-----IFIQLFRTLFSV-----INN SHN-----	140
		: : : : : : : : : : : : : : : : : : : : :	
Db	142	MKD HDDKEATPVFRALIKDILAIPCGKGWNQNLKKEARLLKIQENDDSMNDEEDENAA	201
Qy	141	KKVQM HMLDL MSSII MEGDGV TQELLG SILINLI PAHKNL NKQS FDLAKVLLKRTVQTIE	200
		: : : : : : : : : : : : : : : :	
Db	202	EKIRKSLIQIATTVITNLD FVQNECLD VLFYHII---NPQRSNFAEARALAE---DIIR	254
Qy	201	ACIANFFNQVLVLGRSSVSDLSEH-----VFDLIQELFAIDPHLLLSV	243
		: : : : : : : : : : : : : :	
Db	255	SCSDNESDTLANSIRSTMTAAAKEGKLPEEFELTGSSNRSKF FEVLRYLHYVSFDLVSGA	314
Qy	244	MPQLEFKLKSNDGEERLAVVRL LAKLFGSKDSDLA-TQNRPLWQCFLGRFNDIHVPVRLE	302
		: : : : : : : :	
Db	315	IQELKFWLQSENEQYRKEAVTVVGMLTRDKHCQFGMDSNDPTWSAFLNASIDQDDSVRHE	374

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OM protein - protein search, using sw model

Run on: July 21, 2006, 21:02:48 ; Search time 327 Seconds
(without alignments)
3668.946 Million cell updates/sec

Title: US-10-679-580A-2
Perfect score: 6650
Sequence: 1 MIKRLKMVVKTfMDMDQDSE.....KLQDLAKKAAPAERQIDLQR 1297

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	6650	100.0	1297	2	Q8NG14_HUMAN	Q8ng14 homo sapien
2	6643	99.9	1297	2	Q68DF7_HUMAN	Q68df7 homo sapien
3	6232.5	93.7	1356	2	Q5F3V3_CHICK	Q5f3v3 gallus gall
4	5851	88.0	1323	2	Q4KLU7_XENLA	Q4klu7 xenopus lae
5	5849	88.0	1323	2	Q4QXM3_XENLA	Q4qxm3 xenopus lae
6	5462	82.1	1122	2	Q6A026_MOUSE	Q6a026 mus musculu
7	4694.5	70.6	1446	2	Q4VA53_MOUSE	Q4va53 mus musculu

8	4682.5	70.4	1447	2	Q9NTI5_HUMAN	Q9nti5	homo sapien
9	4682.5	70.4	1483	2	Q9Y2I5_HUMAN	Q9y2i5	homo sapien
10	4678	70.3	1262	2	Q5F3U9_CHICK	Q5f3u9	gallus gall
11	4675.5	70.3	1446	2	Q7TSS4_MOUSE	Q7tss4	mus musculu
12	4652.5	70.0	1391	2	Q9Y451_HUMAN	Q9y451	homo sapien
13	4638.5	69.8	1448	2	Q498H0_XENLA	Q498h0	xenopus lae
14	4593	69.1	1199	2	Q5U241_XENLA	Q5u241	xenopus lae
15	4350	65.4	851	2	Q9Y4D4_HUMAN	Q9y4d4	homo sapien
16	4126.5	62.1	1438	2	Q4SG13_TETNG	Q4sg13	tetraodon n
17	3712.5	55.8	1191	2	Q80TM8_MOUSE	Q80tm8	mus musculu
18	3686	55.4	912	2	Q5R3S3_HUMAN	Q5r3s3	homo sapien
19	2946	44.3	584	2	Q8VDS0_MOUSE	Q8vds0	mus musculu
20	2842	42.7	600	2	Q8N7J4_HUMAN	Q8n7j4	homo sapien
21	2838	42.7	600	2	Q2TTR5_HUMAN	Q2ttr5	homo sapien
22	2612.5	39.3	965	2	Q4QXM2_XENLA	Q4qxm2	xenopus lae
23	2456.5	36.9	701	2	Q8BJ18_MOUSE	Q8bj18	mus musculu
24	2118.5	31.9	824	2	Q8BLH6_MOUSE	Q8blh6	mus musculu
25	2034	30.6	529	2	Q8IXT6_HUMAN	Q8ixt6	homo sapien
26	2033	30.6	454	2	Q4T0S9_TETNG	Q4t0s9	tetraodon n
27	2030.5	30.5	1130	2	Q7PRK5_ANOGA	Q7prk5	anopheles g
28	1911	28.7	1218	2	Q9V646_DROME	Q9v646	drosophila
29	1744.5	26.2	432	2	Q7SXH3_BRARE	Q7sxh3	brachydanio
30	1715	25.8	333	2	Q96DB6_HUMAN	Q96db6	homo sapien
31	1047	15.7	242	2	Q6TRW4_RAT	Q6trw4	rattus norv
32	999	15.0	198	2	Q9D337_MOUSE	Q9d337	mus musculu
33	997.5	15.0	533	2	Q5W0K8_HUMAN	Q5w0k8	homo sapien
34	925.5	13.9	202	2	Q4SZB7_TETNG	Q4szb7	tetraodon n
35	856.5	12.9	1561	2	Q5VMT5_ORYSA	Q5vmt5	oryza sativ
36	785.5	11.8	1250	2	Q4P823_USTMA	Q4p823	ustilago ma
37	779	11.7	1205	1	PDS5_SCHPO	Q9hff5	schizosacch
38	769.5	11.6	1638	2	Q9FIL0_ARATH	Q9fil0	arabidopsis
39	725.5	10.9	1279	2	Q55KR8_CRYNE	Q55kr8	cryptococcu
40	725.5	10.9	1279	2	Q5KAQ6_CRYNE	Q5kaq6	cryptococcu
41	701.5	10.5	1481	2	Q2UB28_ASPOR	Q2ub28	aspergillus
42	696	10.5	1690	2	Q60YT4_CAEBR	Q60yt4	caenorhabdi
43	690.5	10.4	1523	2	Q4I755_GIBZE	Q4i755	gibberella
44	685.5	10.3	1492	2	Q4WZI1_ASPFU	Q4wzi1	aspergillus
45	673.5	10.1	1596	2	Q9UVY6_SORMA	Q9uvy6	sordaria ma

ALIGNMENTS

RESULT 1

Q8NG14_HUMAN

ID Q8NG14_HUMAN PRELIMINARY; PRT; 1297 AA.

AC Q8NG14;

DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.

DT 01-OCT-2002, sequence version 1.

DT 07-FEB-2006, entry version 13.

DE SCC-112.

GN Name=SCC-112;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX PubMed=15019998; DOI=10.1016/j.gene.2003.12.013;

RA Kumar D., Sakabe I., Patel S., Zhang Y., Ahmad I., Gehan E.A.,

RESULT 2

Q68DF7 HUMAN

ID Q68DF7 HUMAN PRELIMINARY; PRT; 1297 AA.

AC Q68DF7;

DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.

DT 11-OCT-2004, sequence version 1.

DT 07-FEB-2006, entry version 12.

DE Hypothetical protein DKFZp686B19246.

GN Name=DKFZp686B19246;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Salivary gland;
 RG The German cDNA Consortium;
 RA Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fobo G., Han M., Wiemann S.;
 RL Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
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 CC -----
 DR EMBL; CR749425; CAH18263.1; -; mRNA.
 DR Ensembl; ENSG00000121892; Homo sapiens.
 DR GO; GO:0005488; F:binding; IEA.
 DR InterPro; IPR011989; ARM-like.
 DR InterPro; IPR000357; HEAT.
 DR Pfam; PF02985; HEAT; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 1297 AA; 146668 MW; 3F6FC3D79DCE238D CRC64;

Query Match 99.9%; Score 6643; DB 2; Length 1297;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1296; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MIKRLKMOVVKT	FMDMDQDSEDEKQ	QYLPALHLASEFFLRNPNKDVRLLVACCLADIFRI	60
Db	1	MIKRLKMOVVKT	FMDMDQDSEDEKQ	QYLPALHLASEFFLRNPNKDVRLLVACCLADIFRI	60
Qy	61	YAPEAPYTSHDKLKDIFLFITRQLKGLEDTKSPQFNRYFYLL	ENLAWVKSYNICFELEDC	120	
Db	61	YAPEAPYTSHDKLKDIFLFITRQLKGLEDTKSPQFNRYFYLL	ENLAWVKSYNICFELEDC	120	
Qy	121	NEIFIQLFRTLFSVINNSHNKKVQMHMLDLMSIIMEGDGVTQELLGSILINLI	PAHKNL	180	
Db	121	NEIFIQLFRTLFSVINNSHNKKVQMHMLDLMSIIMEGDGVTQELLDSILINLI	PAHKNL	180	
Qy	181	NKQSFDLAKVLLKRTVQTI	EACIANFFNQVLVLRSSVSDLSEHVFDLIQELFAIDPHLL	240	
Db	181	NKQSFDLAKVLLKRTVQTI	EACIANFFNQVLVLRSSVSDLSEHVFDLIQELFAIDPHLL	240	
Qy	241	LSVMPQLEFKLKSNDGEERLAVVRL	LAKLFGSKDSDLATQNRPLWQCFLGRFNDIHVPVR	300	
Db	241	LSVMPQLEFKLKSNDGEERLAVVRL	LAKLFGSKDSDLATQNRPLWQCFLGRFNDIHVPVR	300	
Qy	301	LESVKFASHCLMNHPDLAKDLTEYLKVRSHDPEEAI	RHDVIVTIITA	AKRDLALVNDQLL	360
Db	301	LESVKFASHCLMNHPDLAKDLTEYLKVRSHDPEEAI	RHDVIVTIITA	AKRDLALVNDQLL	360
Qy	361	GFVRERTLDKRWRVRKEAMMGLAQLYKKYCLHGEAGKEAAEKVSWIKDKLLHIYYQNSID	420		
Db	361	GFVRERTLDKRWRVRKEAMMGLAQLYKKYCLHGEAGKEAAEKVSWIKDKLLHIYYQNSID	420		
Qy	421	DKLLVEKIFAQYLVP	HNLETEERMKCLYLYASLDPNAVKALNEMWKCQNMLRSHVRELL	480	
Db	421	DKLLVEKIFAQYLVP	HNLETEERMKCLYLYASLDPNAVKALNEMWKCQNMLRSHVRELL	480	
Qy	481	DLHKQPTSEANCSAMFGKLMTIAKNLPDPGKAQDFVKKFNQVLGDDEKLRSQLELLISPT	540		
Db	481	DLHKQPTSEANCSAMFGKLMTIAKNLPDPGKAQDFVKKFNQVLGDDEKLRSQLELLISPT	540		

Qy	541	CSCQADICVREIARKLANPKQPTNPFLEMKVFLLERIAPVHIDSEAI SALVKLMNKSIE	600
Db	541	CSCQADICVREIARKLANPKQPTNPFLEMKVFLLERIAPVHIDSEAI SALVKLMNKSIE	600
Qy	601	GTADDEEEGVSPDTAIRSGLELLKVLSTHPTSFHSAETYESLLQCLRMEDDKVAEAAIQ	660
Db	601	GTADDEEEGVSPDTAIRSGLELLKVLSTHPTSFHSAETYESLLQCLRMEDDKVAEAAIQ	660
Qy	661	IFRNTGHKIIETDLPIRSTLIPILHQKAKRGTPHQAKQAVHCHAI FTNKEVQLAQIFEP	720
Db	661	IFRNTGHKIIETDLPIRSTLIPILHQKAKRGTPHQAKQAVHCHAI FTNKEVQLAQIFEP	720
Qy	721	LSRSLNADVPEQLITPLVSLGHISMLAPDQFASPMKSVVANFIVKDLLMNDRSTGEKNGK	780
Db	721	LSRSLNADVPEQLITPLVSLGHISMLAPDQFASPMKSVVANFIVKDLLMNDRSTGEKNGK	780
Qy	781	LWSPDEEVSPEVLAKVQAIKLLVRWLLGMKNQSKSANSTLRLLSAMLVSEGDLTEQKRI	840
Db	781	LWSPDEEVSPEVLAKVQAIKLLVRWLLGMKNQSKSANSTLRLLSAMLVSEGDLTEQKRI	840
Qy	841	SKSDMSRLRLAAGSAIMKLAQEP CYHEIITPEQFQLCALVINDECYQVRQIFAQKLHKAL	900
Db	841	SKSDMSRLRLAAGSAIMKLAQEP CYHEIITPEQFQLCALVINDECYQVRQIFAQKLHKAL	900
Qy	901	VKLLLPLEYMAIFALCAKDPVKERRAHARQCLLKNI SIRREYIKQNPMA TEKLLSLLPEY	960
Db	901	VKLLLPLEYMAIFALCAKDPVKERRAHARQCLLKNI SIRREYIKQNPMA TEKLLSLLPEY	960
Qy	961	VVPYMIHLLAHDPDFTRSQDQDQLRDIKECLWFMLEVLMTKNENNSHAFMKKMAENIKLT	1020
Db	961	VVPYMIHLLAHDPDFTRSQDQDQLRDIKECLWFMLEVLMTKNENNSHAFMKKMAENIKLT	1020
Qy	1021	RDAQSPDESKTNEKLYTVCDAVLCVINSKSALCNADSPKDPVLPMKFFTQPEKDFCNDKS	1080
Db	1021	RDAQSPDESKTNEKLYTVCDAVLCVINSKSALCNADSPKDPVLPMKFFTQPEKDFCNDKS	1080
Qy	1081	YISEETRVLTLTGKPKPAGVLGAVNKPLSATGRKPYVRSTGTETGSNINVNSELNPSTGN	1140
Db	1081	YISEETRVLTLTGKPKPAGVLGAVNKPLSATGRKPYVRSTGTETGSNINVNSELNPSTGN	1140
Qy	1141	RSREQSSEAAETGVSENEENPVRIISVTPVKNI DPVKNKEINSDQATQGNISSDRGKKRT	1200
Db	1141	RSREQSSEAAETGVSENEENPVRIISVTPVKNI DPVKNKEINSDQATQGNISSDRGKKRT	1200
Qy	1201	VTAAGAENIQKTDKVDSESGPPAPSKPRRGRRPKSESQGNATKNDDL NKPINKGRKRAA	1260
Db	1201	VTAAGAENIQKTDKVDSESGPPAPSKPRRGRRPKSESQGNATKNDDL NKPINKGRKRAA	1260
Qy	1261	VGQESPGGLEAGNAKAPKLQDLAKKAAPAERQIDLQR	1297
Db	1261	VGQESPGGLEAGNAKAPKLQDLAKKAAPAERQIDLQR	1297

RESULT 3

Q5F3V3_CHICK

ID Q5F3V3_CHICK PRELIMINARY; PRT; 1356 AA.

AC Q5F3V3;

DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.

DT 15-MAR-2005, sequence version 1.

DT 07-FEB-2006, entry version 4.

DE Hypothetical protein.

Query Match 93.7%; Score 6232.5; DB 2; Length 1356;
Best Local Similarity 93.5%; Pred. No. 0;
Matches 1213; Conservative 36; Mismatches 46; Indels 3; Gaps 3;

http://es/ScoreAccessWeb/GetItem.action?AppId=10679580&seqId=567838&ItemName=us-10-679-580a... 8/6/2006

ID Q4KLU7_XENLA PRELIMINARY; PRT; 1323 AA.
AC Q4KLU7;
DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 02-AUG-2005, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE Hypothetical protein.
OS *Xenopus laevis* (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; *Xenopus*; *Xenopus*.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Oocytes;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for *Xenopus* research: The NIH *Xenopus*
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Oocytes;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Oocytes;
RA Klein S., Gerhard D.S.;
RL Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; BC098992; AAH98992.1; -; mRNA.
KW Hypothetical protein.
SQ SEQUENCE 1323 AA; 149527 MW; CC1C1F80CFD0FFBD CRC64;

Query Match 88.0%; Score 5851; DB 2; Length 1323;
Best Local Similarity 87.6%; Pred. No. 5.8e-307;
Matches 1138; Conservative 73; Mismatches 78; Indels 10; Gaps 7;

Qy	1	MIKRLKMMVVKT	FMDMDQDSEEEKQY	LPLALHLASEF	FLRNPKNKDVRLL	VACCLADIFRI	60																																																						
Db	33	VVKRLKMMVVKT	FMDMDQDSEEEKQY	LPLALHLSSD	FLRNPKNKDVRLL	VACCLADIFRI	92																																																						
Qy	61	YAPEAPY	TSHDKLKDIFL	ITRQLKGLED	TKSPQFNRYFY	LLENLAWVKS	SYNICFELED	120																																																					
Db	93	YAPEAPY	TSHDKLKEIFL	ITRQLKGLED	TKSPQFNRYFY	LLENLAWVKS	SYNICFELED	152																																																					
Qy	121	NEIFIQL	FRTLFSVIN	NSHNKQV	MMHMLDLM	SSIIM	EGDGV	TQELLGSILINLI	PAHKNL	180																																																			
Db	153	NEIFIQL	FKTLFSVIN	NSHNQKV	MMHMLDLM	SSITM	EGDGV	TQEQLDSILINLI	SAHKNL	211																																																			
Qy	181	NKQSF	DLAKVLLK	RTVQ	TI	EACIANF	NQV	LV	LGRSSV	SDLSE	HVFD	LIQEL	FAID	PHLL	240																																														
Db	213	NKQAF	DLAKVLLK	RTAQ	TI	EPCIANF	NQV	LV	LGRSSV	SDLSE	HVFD	LIQEL	FAID	PHLL	272																																														
Qy	241	LSVMP	QLEFKL	KSND	GEER	LAVVR	LLAKL	FGSK	DS	DLATQ	NRPL	WQCF	LGR	FNDI	HVPVR	300																																													
Db	273	LSVMP	QLEFKL	KSND	GEER	LAVVR	LLAKL	FGSK	DS	DLATQ	NRPL	WQCF	LGR	FNDI	HVPVR	332																																													
Qy	301	LESVK	FASHCL	MNHP	DLAK	DLTEY	LKVR	SHD	PEEAI	RHDV	IVTI	ITAA	KRDL	ALVND	QLL	360																																													
Db	333	LESVK	FASHCL	MNHP	DLAK	DLTEF	LKVR	SHD	PEEAI	RHDV	IVTI	ITAA	KKDL	FLVND	QLL	392																																													
Qy	361	GFVR	ERTLDK	RWRVR	KEAM	GLAQ	LYKKY	CLH	GEG	KDAE	KVSWI	KDKL	LHI	YYQ	NSID	420																																													
Db	393	GFVR	ERTLDK	RWRVR	KEAM	GLAQ	LYKKY	CLH	GEG	KDAE	KVSWI	KDKL	LHI	YYQ	NSID	452																																													
Qy	421	DKLL	VEKIFA	QYLV	PHNLE	TEERM	KCLY	YLYA	SLDP	NAVK	ALNEM	WKCQ	NMLR	SHV	RELL	480																																													
Db	453	DKLL	VEKIFA	QQLV	PHNLE	TEERM	KCLY	YLYA	SLDP	NAVK	ALNEM	WKCQ	NMLR	SHV	RELL	512																																													
Qy	481	DLHK	QPTSE	ANCSA	MFGK	LMTI	AKNL	PD	PGKA	QDFV	KKFN	QVLG	DEKL	RSQ	LELLIS	PT	540																																												
Db	513	DLHK	QPTSE	ANTTA	MF	AKLMT	VAKNL	PD	PGKA	QDFV	KKFN	QVLG	EDGE	KLRSQ	LEVLIS	PS	572																																												
Qy	541	C	SCQADIC	VREI	ARKLAN	PKQPT	NPF	LEMV	KFL	LRIAP	VHID	SEAI	SALV	KLMN	KSIE	600																																													
Db	573	C	SCQADV	CV	RDIA	RKVAN	PKQPT	NPF	LEMV	KFL	LRIAP	VHID	SEAI	SALV	KLMN	KSIE	632																																												
Qy	601	GTAD	DEEEGV	SPDTA	IRSG	LELLK	VLSF	THPT	SFHS	AETY	ESLL	QCL	RMED	DKVA	EAAIQ	660																																													
Db	633	GTAD	DEEEGV	SP	SAIR	AGLELLK	VLSF	THPT	SFHS	DETY	ESLL	QCL	RMED	DKVA	EAAIQ	692																																													
Qy	661	I	FRNTGH	KIET	DL	PQIR	STLI	PIL	HQAK	RGTP	HQAK	QAVH	CIHAI	FTN	KEV	QLAQIF	EP	720																																											
Db	693	I	FRNTGH	RIET	DL	PQIR	SALI	PIL	HQAK	RGTP	HQAK	QAVH	CIHSI	FSN	KEV	QLAQIF	EP	752																																											
Qy	721	L	S	RS	LNAD	VPEQL	ITPL	VSL	GHIS	MLAP	DQFAS	PMKSV	VANF	IVK	DL	LMNDR	STGE	KNGK	780																																										
Db	753	L	S	RS	LNAD	VPEQL	VTPL	VSL	GHIS	MLAP	DQFAS	PMKSV	VANF	IVK	DL	LMNDR	SNGD	KNGK	812																																										
Qy	781	L	W	S	P	D	E	E	E	V	S	P	E	V	L	A	K	Q	A	I	K	L	L	V	R	W	L	G	M	K	N	N	Q	S	K	S	A	N	S	T	L	R	L	L	S	A	M	L	V	S	E	G	D	L	T	E	Q	K	R	I	840
Db	813	L	W	C	P	D	E	E	E	V	S	P	E	V	L	A	K	Q	A	I	K	L	L	V	R	W	L	G	M	K	N	N	Q	S	K	S	A	N	S	T	L	R	L	L	S	A	M	L	V	S	E	G	D	L	T	E	Q	K	R	I	872
Qy	841	S	K	S	D	M	S	R	L	R	L	A	A	G	S	A	I	M	K	L	A	Q	E	P	C	Y	H	E	I	T	P	E	Q	F	Q	L	C	A	L	V	I	N	D	E	C	Y	Q	V	R	Q	I	F	A	Q	K	L	H	K	A	L	900
Db	873	S	K	S	D	M	S	R	L	R	L	A	A	G	A	I	M	K	L	A	Q	E	P	C	Y	H	E	I	T	P	E	Q	F	Q	L	C	A	L	V	I	N	D	E	C	Y	Q	V	R	Q	I	F	A	Q	K	L	H	K	A	L	932	
Qy	901	V	K	L	L	L	P	L	E	Y	M	A	I	F	A	L	C	A	K	D	P	V	K	E	R	R	A	H	A	R	Q	C	L	L	K	N	I	S	I	R	R	E	Y	I	K	O	N	P	M	A	T	E	K	L	L	S	L	P	E	Y	960